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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:18 ; Search time 37.6503 Seconds
(without alignments)
4236.886 Million cell updates/sec

Title: US-09-918-508-4_COPY_32_1036

Perfect score: 5159

Sequence: 1 GIEDKSGLLVGSVDLETK.....AEQLYREVSRRFFNSPSTES 1005

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5159	100.0	1036	23	ABG70782
2	5159	100.0	1036	24	AAE33693
3	5001	96.9	1092	23	AAO22567
4	5001	96.9	1092	23	ABG91150
5	2685.5	52.1	1132	21	AAG47090
6	2685.5	52.1	1176	21	AAG47089
7	2685.5	52.1	1176	23	ABG70781
8	2685.5	52.1	1176	24	AAE33692
9	2685.5	52.1	1238	21	AAG47088

10	2674	51.8	1173	23	AAO22568	Wooden leg (WOL) g
11	2674	51.8	1173	23	ABB93625	Herbicidally activ
12	2481.5	48.1	1057	23	ABG70783	A. thaliana cytoki
13	2475.5	48.0	1057	23	AAO22558	Wooden leg (WOL) g
14	2475.5	48.0	1057	23	AAO22570	Wooden leg (WOL) g
15	2475.5	48.0	1057	24	AAE33694	Arabidopsis thalia
16	2470.5	47.9	1057	24	AAE33696	Arabidopsis thalia
17	2467.5	47.8	1057	24	AAE33695	Herbicidally activ
18	1487.5	28.8	600	23	ABB91688	Eucalyptus grandis
19	975	18.9	412	21	AAE33695	Eucalyptus grandis
20	937.5	18.2	426	21	AAE33695	Eucalyptus grandis
21	867.5	16.8	274	23	AAO22561	Wooden leg (WOL) g
22	849.5	16.5	289	23	AAO22563	Wooden leg (WOL) g
23	684.5	13.3	1298	19	AAW68522	N. crassa osp pro
24	684.5	13.3	1298	20	AAW68522	os1+p amino acid s
25	682.5	13.2	1281	20	AAW68522	os1 histidine kina
26	682.5	13.2	1298	20	AAW68522	os1 histidine kina
27	651	12.6	1018	21	AAE33694	Eucalyptus grandis
28	640.5	12.4	1081	20	AAE33694	cos-1 histidine ki
29	640.5	12.4	1081	20	AAW81600	Candida albicans C
30	620.5	12.0	922	22	AAW81600	Histidine protein k
31	620.5	12.0	922	22	AAW81600	Histidine protein k
32	615.5	11.9	922	22	AAW81600	Histidine protein k
33	600	11.6	170	21	AAW81600	Eucalyptus grandis
34	594.5	11.5	950	23	ABB93422	Herbicidally activ
35	563	10.9	2150	23	AAO22566	Wooden leg (WOL) g
36	560	10.9	971	20	AAW88480	Candida albicans h
37	560	10.9	2471	20	AAW88481	Candida albicans h
38	557.5	10.8	1122	23	ABB92150	Herbicidally activ
39	543	10.5	816	21	AAE33694	Eucalyptus grandis
40	534.5	10.4	666	24	AAO26994	Pseudomonas aerugi
41	534.5	10.4	709	24	AAO26993	Pseudomonas aerugi
42	534.5	10.4	719	24	AAO26992	Pseudomonas aerugi
43	534.5	10.4	802	24	AAO26991	Pseudomonas aerugi
44	534.5	10.4	870	24	AAO26990	Pseudomonas aerugi
45	534.5	10.4	874	24	AAO26989	Pseudomonas aerugi

ALIGNMENTS

RESULT 1

ABG70782

ID ABG70782 standard; Protein; 1036 AA.

XX

AC ABG70782;

XX 09-DEC-2002 (first entry)

XX A. thaliana cytokinin receptor, AHK3, protein.

DE AHK3; plant; antagonist; agonist; cytokinin receptor;

KW receptor; signal transduction; histidine kinase; hormone; cell division;

KW cell differentiation; agriculture; growth regulator; harvest.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX

FH Key Location/Qualifiers

FT Region 32..1036

FT /note= "This region is specifically claimed in Claim 1"

XX

PN EP1241182-A2.

XX

PD 18-SEP-2002.

XX

PF 13-MAR-2002; 2002EP-0005749.

XX

PR 15-MAR-2001; 2001JP-0073812.

PR 29-JUN-2001; 2001JP-0198639.

PR 29-JUN-2001; 2001JP-0198640.

XX

PA (SUMO) SUMITOMO CHEM CO LTD.

XX

PI Kakimoto T, Higuchi M, Inoue T;
XX WPI; 2002-693041/75.
DR N-PSDB; ABS54451.
XX
PT Analyzing agonist or antagonist activity of a substance for use as a
PT plant growth regulator, comprises measuring intracellular signal
PT transduction from a cytokinin receptor expressed in a cell contacted
PT with the test substance -
XX
PS Claim 1; Page 32-34; 47pp; English.
XX
CC The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
CC presented is the A. thaliana cytokinin receptor, AHK3, protein.
XX
SQ Sequence 1036 AA;

Query Match 100.0%; Score 5159; DB 23; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIEDKSGLLVSGVDLEKTKMTTLKKKNKMWFWNKISSGLKIPSFYSYQFLGSKVFNKAW 60
Db |||||||
32 GIEDKSGLLVSGVDLEKTKMTTLKKKNKMWFWNKISSGLKIPSFYSYQFLGSKVFNKAW 91
QY 61 WRKLVVWVFWVLVSIWTFWFSSQAMEKREKTKETLASCMDERARMQLQDFNVSMNHVQAM 120
Db |||||||
92 WRKLVVWVFWVLVSIWTFWFSSQAMEKREKTKETLASCMDERARMQLQDFNVSMNHVQAM 151
QY 121 SILISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEEFERQOGWTI 180
Db |||||||
152 SILISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEEFERQOGWTI 211
QY 181 RKMYSLEQNPHVKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVLR 240
Db |||||||
212 RKMYSLEQNPHVKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVLR 271
QY 241 ARSSGKGVLTAPFPLIKTNRLGVILTFVAVYKRDLPNATPKERIEATNGYLGGVFDIESL 300
Db |||||||
272 ARSSGKGVLTAPFPLIKTNRLGVILTFVAVYKRDLPNATPKERIEATNGYLGGVFDIESL 331
QY 301 VENLLOQLASKQTILVNVDITNHSQPISMYGTNVSDGLERVSPLIFGDPRLRKHEMRCR 360
Db |||||||
332 VENLLOQLASKQTILVNVDITNHSQPISMYGTNVSDGLERVSPLIFGDPRLRKHEMRCR 391
QY 361 FKQKPPWPVLSMVTSGILVIALVAHIIHATVSRIHKVEEDCKMKQLKKAEAAADVAK 420
Db |||||||
392 FKQKPPWPVLSMVTSGILVIALVAHIIHATVSRIHKVEEDCKMKQLKKAEAAADVAK 451
QY 421 SQFLATVSHEIRTPMNGVLGMLHMLMDTELDTVTDQDYVRTAQSGKALVSLINEVLDOAK 480
Db |||||||
452 SQFLATVSHEIRTPMNGVLGMLHMLMDTELDTVTDQDYVRTAQSGKALVSLINEVLDOAK 511
QY 481 IESGKLEIEVRFDLRGILDDVLSLFSSKSKQKGVELAVTSDRVPDMLIGDPGRFRQIL 540
Db |||||||
512 IESGKLEIEVRFDLRGILDDVLSLFSSKSKQKGVELAVTSDRVPDMLIGDPGRFRQIL 571

QY 541 TNLGMNSIKFTEKGHIFVTVHLVDELFPESIDGETASSPESTLSGLPVADRQSRWENFKAF 600
Db |||||||
572 TNLGMNSIKFTEKGHIFVTVHLVDELFPESIDGETASSPESTLSGLPVADRQSRWENFKAF 631
QY 601 SNGHRSFEPSPDINLIVSVEDTGVGIPVEAQSRIFTFFMQVGPSPISRTHGGTGIGLSI 660
Db |||||||
632 SNGHRSFEPSPDINLIVSVEDTGVGIPVEAQSRIFTFFMQVGPSPISRTHGGTGIGLSI 691
QY 661 SKCLVGLMKGEIGFSSSTPKVGSTFTFTAVFSNGMQPAERKNDNNQPIFSEFRGMKAVVVD 720
Db |||||||
692 SKCLVGLMKGEIGFSSSTPKVGSTFTFTAVFSNGMQPAERKNDNNQPIFSEFRGMKAVVVD 751
QY 721 HRPARAKVSWYHFQRLGIRVEVPRVEQALHYLKIGTTTNNMILIEQEIWNREADDFIKK 780
Db |||||||
752 HRPARAKVSWYHFQRLGIRVEVPRVEQALHYLKIGTTTNNMILIEQEIWNREADDFIKK 811
QY 781 LQKDPLFLSPKLILLANSVSESSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIRE 840
Db |||||||
812 LQKDPLFLSPKLILLANSVSESSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIRE 871
QY 841 PPQHKGPPALILRNLILGRKILIVDDNNVNLRAAGALKKYGADVCAESGKKAISLLKP 900
Db |||||||
872 PPQHKGPPALILRNLILGRKILIVDDNNVNLRAAGALKKYGADVCAESGKKAISLLKP 931
QY 901 PHEFDACFMDIQMBMDGFEATRIRDMEEEMNKRIKNGEALIVENGKTSWHLPLVLA 960
Db |||||||
932 PHEFDACFMDIQMBMDGFEATRIRDMEEEMNKRIKNGEALIVENGKTSWHLPLVLA 991
QY 961 ADVIQATHEECLKCGMDGYVSKPFPAEQLYREVSRFFNSPSPDTS 1005
Db |||||||
992 ADVIQATHEECLKCGMDGYVSKPFPAEQLYREVSRFFNSPSPDTS 1036

RESULT 2
AAE333693
ID AAE333693 standard; Protein; 1036 AA.
XX
AC AAE333693;
XX
DT 16-APR-2003 (first entry)
XX
DE Arabidopsis thaliana histidine kinase 3 (AHK3) protein.
XX
KW Shoot formation; senescence; transgenic; transgenic plant; agriculture;
KW cell proliferation; shoot meristem formation; leaf development; AHK;
KW photosynthesis; histidine kinase; enzyme.
XX
OS Arabidopsis thaliana.
XX
PN WO200299079-A2.
XX
PD 12-DEC-2002.
XX
PF 06-JUN-2002; 2002WO-US18066.
XX
PR 06-JUN-2001; 2001US-296554P.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Sheen J, Hwang I;
XX
DR WPI; 2003-140613/13.
XX
PT Increasing yield in plant, increasing shoot formation in a plant, or
PT delaying senescence in a plant such as wheat, rice, maize, barley,
PT potato, by using transgenes that regulate cytokinin response -
XX
PS Disclosure; Page 78-80; 87pp; English.
XX
CC The present invention relates to a novel method of increasing yield in a
CC plant, increasing shoot formation or delaying senescence in a plant. The
CC method involves introducing into plant cells, a transgene having a B-type

CC response regulator operably linked to a promoter functional in plant
CC cells to yield transformed plant cells or whose expression reduces the
CC expression of A-type response regulator in the cells of the plant and
CC regenerating a plant from the transformed cells. The method is useful
CC for increasing the yield in a plant, increasing the shoot formation or
CC delaying senescence in a plant such as wheat, rice, maize, barley,
CC potato, tomato, soybean, oat, cotton and sunflower. The method
CC is useful for variety of agricultural and commercial purposes including
CC improving and enhancing photosynthesis, promoting cell proliferation,
CC shoot meristem formation, promoting leaf development, increasing crop
CC yields, improving crop and ornamental quality and reducing agricultural
CC production costs. The present sequence is Arabidopsis thaliana histidine
CC kinase 3 (AHK3) protein. This sequence is used to illustrate the method
CC of the invention.

XX Sequence 1036 AA;

Query Match 100.0%; Score 5159; DB 24; Length 1036;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1005; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEDKSGLLVSGVDLEKTKMTTLKKKNMFWFNKISSSGLKIPFSYQDPLGSKVFNKAW 60
Db |||||
QY 61 WRKLVVVVWVFWVLVSIWTFWYFSSQAMEKKEKTLASCMCDERARMLOQDQFNVMNHVQAM 120
Db |||||
QY 92 WRKLVVVVWVFWVLVSIWTFWYFSSQAMEKKEKTLASCMCDERARMLOQDQFNVMNHVQAM 151
Db |||||
QY 121 SILISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEFEFERQQGWTI 180
Db |||||
QY 152 SILISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEFEFERQQGWTI 211
Db |||||
QY 181 RKMYSLEQNPHKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVS LDM LSGKEDRENVL 240
Db |||||
QY 212 RKMYSLEQNPHKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVS LDM LSGKEDRENVL 271
Db |||||
QY 241 ARSSGKGLTAPPLIKTNRLGVILTFVAVYKRDLP SNATPKERIEATNGYLGGVFDIESL 300
Db |||||
QY 272 ARSSGKGLTAPPLIKTNRLGVILTFVAVYKRDLP SNATPKERIEATNGYLGGVFDIESL 331
Db |||||
QY 301 VENLLQQLASKOTILNVVYDITNHSQIPSMYGFNV SADGLERSVPLIFGDPLRKHEMRCR 360
Db |||||
QY 332 VENLLQQLASKOTILNVVYDITNHSQIPSMYGFNV SADGLERSVPLIFGDPLRKHEMRCR 391
Db |||||
QY 361 FKQKPPWPVLSMVTSGILVIALLVAHIIHATVSRHKVEEDCKMKQLKKKAEAAADVAK 420
Db |||||
QY 392 FKQKPPWPVLSMVTSGILVIALLVAHIIHATVSRHKVEEDCKMKQLKKKAEAAADVAK 451
Db |||||
QY 421 SQFLATVSHEIRTPMNGVGLM LMLMDTDLVDTQDDYVRTAQASGKALVSLINEVLDQAK 480
Db |||||
QY 452 SQFLATVSHEIRTPMNGVGLM LMLMDTDLVDTQDDYVRTAQASGKALVSLINEVLDQAK 511
Db |||||
QY 481 IESGKLEEVRFDLRGILDVLSLFSKSKQKGVELAVYISDRVPM LIGDPRFRQIL 540
Db |||||
QY 512 IESGKLEEVRFDLRGILDVLSLFSKSKQKGVELAVYISDRVPM LIGDPRFRQIL 571
Db |||||
QY 541 TNLMGNSIKFTEKGHIFVTVHLVDEL FESIDGETASSPESTLSGLPVADRQRSWENFKAF 600
Db |||||
QY 572 TNLMGNSIKFTEKGHIFVTVHLVDEL FESIDGETASSPESTLSGLPVADRQRSWENFKAF 631
Db |||||
QY 601 SSNGHRSFEPSPDINLIVSVEDTG VIGIPVEAQSRIFTFPMQVGPSISRTHGGTGIGLSI 660
Db |||||
QY 632 SSNGHRSFEPSPDINLIVSVEDTG VIGIPVEAQSRIFTFPMQVGPSISRTHGGTGIGLSI 691
Db |||||
QY 661 SKCLVGLMKGEIGFSSTPKVGSTFTTAVFSGM QPAERKNDNNQPIFSEFRGMKAVVVD 720
Db |||||
QY 692 SKCLVGLMKGEIGFSSTPKVGSTFTTAVFSGM QPAERKNDNNQPIFSEFRGMKAVVVD 751
Db |||||
QY 721 HRPARAKVSWYHFQRLGIRVEVVRVEQALHYLKIGTTTTNNMILIEQEIWNREADDFIKK 780
Db |||||
QY 752 HRPARAKVSWYHFQRLGIRVEVVRVEQALHYLKIGTTTTNNMILIEQEIWNREADDFIKK 811
Db |||||

QY 781 LQKDPLFLSPKILLANSVSESSISEALCTGIDPPIVIVKPLRASM LAAATLQRLGIGIRE 840
Db |||||
QY 812 LQKDPLFLSPKILLANSVSESSISEALCTGIDPPIVIVKPLRASM LAAATLQRLGIGIRE 871
Db |||||
QY 841 PPQHKGPALILRNLLGRKILIVDDNNVNL RVAAGALKKYGADVCAESGIKAISLLKP 900
Db |||||
QY 872 PPQHKGPALILRNLLGRKILIVDDNNVNL RVAAGALKKYGADVCAESGIKAISLLKP 931
Db |||||
QY 901 PHEFDACFMDIQPEMDGF EATRRI RDMEEEMNKRIKNGEALIVENGKNTSWHLPVLAMT 960
Db |||||
QY 932 PHEFDACFMDIQPEMDGF EATRRI RDMEEEMNKRIKNGEALIVENGKNTSWHLPVLAMT 991
Db |||||
QY 961 ADVIQATHEECLKCGMDGYVSKPFEAEQLYREVSRFFNSPDTES 1005
Db |||||
QY 992 ADVIQATHEECLKCGMDGYVSKPFEAEQLYREVSRFFNSPDTES 1036
Db |||||

RESULT 3
AAO22567

ID AAO22567 standard; Protein; 1092 AA.

XX AAO22567;

DT 28-OCT-2002 (first entry)

XX Wooden leg (WOL) gene related protein SEQ ID No 18.

XX Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.

XX Arabidopsis thaliana.

PN WO200244337-A2.

XX 06-JUN-2002.

PF 29-NOV-2001; 2001WO-US45053.

PR 29-NOV-2000; 2000US-253739P.

XX (UINY) UNIV NEW YORK STATE.

PA (HELA/) HELARIUTTA Y.

PA (MAHO/) MAHONEN A P.

PA (BONK/) BONKE A W M.

PA (KAUP/) KAUPPINEN L.

PA (RIIK/) RIIKONEN M.

XX Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;

PI Benfey PN;

XX WPI; 2002-599423/64.

XX Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set

PT of asymmetric cell divisions that establish vascular tissue in root and

PT hypocotyl development, useful for improving agronomically valuable

PT plants -

XX Example 1; Page 157-161; 187pp; English.

PS The invention relates to an isolated WOODEN LEG (WOL) polypeptide,

XX comprising 15 contiguous amino acids of a fully defined Arabidopsis

CC WOODEN LEG protein sequence of 1057 amino acids as given in the

endogenous WOL genes, WOL mutant alleles and/or WOL expression products in cultivars as compared to wild-type plants. They can also be used as markers for linkage analysis of qualitative trait loci. The WOL protein and/or antibodies can be used as diagnostic reagents in immunoassays to detect expression of the WOL gene in cultivars and wild-type plants. The WOL protein, its encoding nucleic acid, and its corresponding antibody are useful for improving agronomically valuable plants e.g., trees. This sequence represents a protein relating to the wooden leg (WOL) protein of the invention.

Sequence 1092 AA;

Db	872	TGIDPPIVIVKPLRASMLAATLQRLGLGIGIREPPQHKGPPALILRNLLGRKILIVDDNN	931
QY	869	VNLRVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMPEMDGFETRIRDM	928
Dd	932	VNLRVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMPEMDGFETRIRDM	991
QY	929	EEMNKRIKNGEALIVENGNKTSWHLPLVAMTADVIQATHEECLKCGMDGY	979
Dd	992	EEMNKRIKNGEALIVENGNKTSWHLPLVAMTADVIQATHEECLKCGMDGY	1042

RESULT 4

ABB91150

ID	ABB91150	standard	Protein	1092 AA

AC ABB91150;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 361.

KW Herbicidal; plant; agriculture; herbicide.

OS *Arabidopsis thaliana*.

XX
PN
WO200210210-A2.

07-FEB-2002.

XX
PF 28-AUG-2001; 2001WO-EP09892.

PR 28-AUG-2001; 2001WO-EP09892.

PA (FARB) BAYER AG.

PI Tietjen K, Weidler M;

DR WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -

PS Claim 5; SEQ ID NO 361; 261pp + Sequence Listing; English.

The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.

Sequence	1092 AA;
SQ	

Query Match 96.9%; Score 5001; DB 23; Length 1092;

Best Local Similarity 96.8%; Pred. No. 0;

Matches 979; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 GIEDKSGLLVGSVGDLEKTKMTTLKKKNKMFWNKISSSGLKIPSFYQFLGSVKFNKAW 60

Db 32 GIEDKSGLLVGSVGDLEKTKMTTLKKKNKMWFNKISSSGLKIPSFYQFLGSVKFNKAW 91

QY 61 WRKLVVVVFWVLVSIWTFWYFSSQAMEKRKETLASMCDERARMLQDQFNVS MNHVQAM 120

Db 92 WRKLVVWVFWVLVSIWTFWFSSQAMEKRKETLASMCDERARMLQDQFNVS MNHVQAM 151

Qy 121 SILISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEREEEFERQOGWTI 180

Db	152	SILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREFERQGWTI	211	OS	Arabidopsis thaliana.
QY	181	RKMYSLEQNPHVKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVL	240	XX	EP1033405-A2.
Db	212	RKMYSLEQNPHVKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVL	271	XX	
QY	241	ARSGKGVLTAPFPLIKTNRLGVILTFPAVKRDLPSNATPKERIEATNGYLGGVFDIESL	300	PD	06-SEP-2000.
Db	272	ARSGKGVLTAPFPLIKTNRLGVILTFPAVKRDLPSNATPKERIEATNGYLGGVFDIESL	331	XX	25-FEB-2000; 2000EP-0301439.
QY	301	VENLLQQLASKQTILVNVYDITNHSQPISMYGTNVSADGLERVSPLIFGDP	358	PR	25-FEB-1999; 99US-0121825.
Db	332	VENLLQQLASKQTILVNVYDITNHSQPISMYGTNVSADGLERVSPLIFGDP	391	PR	05-MAR-1999; 99US-0123180.
QY	359	-----CRFKQKPPWPVLSMVTSGILVIALVAHI	388	PR	09-MAR-1999; 99US-0123548.
Db	392	YLQLAHTYVCNFFLFARIQVLTFCCELLPLCRFKQKPPWPVLSMVTSGILVIALVAHI	451	PR	23-MAR-1999; 99US-0125788.
QY	389	IHATVSRIHKVEEDCDKMKQLKKKAAEADVAKSQFLATVSHEIRTPMNGVLGMLHMLMDT	448	PR	25-MAR-1999; 99US-0126264.
Db	452	IHATVSRIHKVEEDCDKMKQLKKKAAEADVAKSQFLATVSHEIRTPMNGVLGMLHMLMDT	511	PR	29-MAR-1999; 99US-0126785.
QY	449	ELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLEBEVRFDLRGLDDVLSLFS	508	PR	01-APR-1999; 99US-0127462.
Db	512	ELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLEBEVRFDLRGLDDVLSLFS	571	PR	06-APR-1999; 99US-0128234.
QY	509	KSQOKGVELAVYISDRVPMGLIGDPGRFRQILTNLMGNSIKFTEKGHIFVTVHLVDELFE	568	PR	08-APR-1999; 99US-0128714.
Db	572	KSQOKGVELAVYISDRVPMGLIGDPGRFRQILTNLMGNSIKFTEKGHIFVTVHLVDELFE	631	PR	16-APR-1999; 99US-0129845.
QY	569	SIDGETASSPESTLSGLPVADQRQSWENFKAFSSNGHRSFEPSPDINLIVS	628	PR	19-APR-1999; 99US-0130077.
Db	632	SIDGETASSPESTLSGLPVADQRQSWENFKAFSSNGHRSFEPSPDINLIVS	691	PR	21-APR-1999; 99US-0130449.
QY	629	PVEAQSRIFTFPMQVGPSISRTHGGTGIGLSISKCLVGLMKEIGFSSTPKVGSTFTFTA	688	PR	23-APR-1999; 99US-0130510.
Db	692	PVEAQSRIFTFPMQVGPSISRTHGGTGIGLSISKCLVGLMKEIGFSSTPKVGSTFTFTA	751	PR	23-APR-1999; 99US-0130891.
QY	689	VFSNGMQPAERKNDNNQPIFSEFRGMKAVVDHRPARAKVSWYHFQRLGIRVEVPRVEQ	748	PR	28-APR-1999; 99US-0131449.
Db	752	VFSNGMQPAERKNDNNQPIFSEFRGMKAVVDHRPARAKVSWYHFQRLGIRVEVPRVEQ	811	PR	30-APR-1999; 99US-0132048.
QY	749	ALHYLKIGTTTVMILIEQIWNREADDFIKKLQKDPFLSPKLILLANSV	808	PR	30-APR-1999; 99US-0132407.
Db	812	ALHYLKIGTTTVMILIEQIWNREADDFIKKLQKDPFLSPKLILLANSV	871	PR	04-MAY-1999; 99US-0132484.
QY	809	TGIDPPVIVKPLRASMLAATLQRLGIGIREPPQHKGPPALILRNLLGRKILIVDDNN	868	PR	05-MAY-1999; 99US-0132485.
Db	872	TGIDPPVIVKPLRASMLAATLQRLGIGIREPPQHKGPPALILRNLLGRKILIVDDNN	931	PR	06-MAY-1999; 99US-0132486.
QY	869	VNLRVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMP	928	PR	07-MAY-1999; 99US-0132487.
Db	932	VNLRVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMP	991	PR	11-MAY-1999; 99US-0132863.
QY	929	EEEMNKRIKNGEALIVENGNKTSWHLPVLAMTADVIQATHEECLKGMDGY	979	PR	11-MAY-1999; 99US-0134256.
Db	992	EEEMNKRIKNGEALIVENGNKTSWHLPVLAMTADVIQATHEECLKGMDGY	1042	PR	14-MAY-1999; 99US-0134218.
RESULT 5				PR	14-MAY-1999; 99US-0134219.
AAG47090				PR	14-MAY-1999; 99US-0134221.
ID		AAG47090 standard; Protein; 1132 AA.		PR	14-MAY-1999; 99US-0134370.
XX				PR	18-MAY-1999; 99US-0134768.
AC		AAG47090;		PR	19-MAY-1999; 99US-0134941.
XX				PR	20-MAY-1999; 99US-0135124.
DT		18-OCT-2000 (first entry)		PR	21-MAY-1999; 99US-0135353.
XX				PR	24-MAY-1999; 99US-0135629.
DE		Arabidopsis thaliana protein fragment SEQ ID NO: 59314.		PR	25-MAY-1999; 99US-0136021.
XX				PR	27-MAY-1999; 99US-0136392.
KW		Protein identification; signal transduction pathway; metabolic pathway;		PR	28-MAY-1999; 99US-0136782.
KW		hybridisation assay; genetic mapping; gene expression control; promoter;		PR	01-JUN-1999; 99US-0137222.
KW		termination sequence.		PR	03-JUN-1999; 99US-0137528.
XX				PR	04-JUN-1999; 99US-0137502.

Db	544	KSQFLATVSHIRTPMNGVLGMLKMLMDTDLDAKQMDYAQTAHSGSKDLTSLINEVLDOA	603	PR	08-APR-1999;	99US-0128714.
QY	480	KIESGKLEIEVRFDLRGILDVLSFSSKSOQKGVELAVYISDRVPDMLIGDPGRFRQI	539	PR	16-APR-1999;	99US-0129845.
Db	604	KIESGRLELENVFPDMRFILDNVSSLSGKANEGIELAVYSSQVPDWWVGDPSPRFRQI	663	PR	19-APR-1999;	99US-0130077.
QY	540	LTNLMGNSIKFT-EKGHIFVTVHLVDELPESIDGETA-----SSPESTLSGLPVA	588	PR	21-APR-1999;	99US-0130449.
Db	664	ITNLVGNISIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSSESGETVSGFPV	723	PR	23-APR-1999;	99US-0130510.
QY	589	DRQSRWENFK-AFSSNGHRSFEPSPPDINLIVSVEDTGVGIPVEAQSRIFTPFMOVGPSI	647	PR	28-APR-1999;	99US-0130891.
Db	724	NAWGSWKNFKTCYSTESQNS-----DQIKLLVTVEDTGVGIPVDAQGRIFTPFMQADSST	778	PR	30-APR-1999;	99US-0131449.
QY	648	SRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTFTAVFSNGMQPAERKNDNNQPI	707	PR	30-APR-1999;	99US-0132048.
Db	779	SRTYGGTGIGLSISKRLVELMQGEMGFVSEPGIGSTFSFTGVFG-----KAETNTSI	830	PR	30-APR-1999;	99US-0132407.
QY	708	-----FSEFRGMKAVVVDHRPARAKVSWYHFQRLGIRVEVVPRVEQALHYLKIGTT	758	PR	04-MAY-1999;	99US-0132484.
Db	831	TKLERFDLAIQFTGLRALVIDNRNIRAETRYELRRLGISADIVSSLRMACTCCISKLE	890	PR	05-MAY-1999;	99US-0132485.
QY	759	TVNMILIEQEIWNREADDFIKKL---QKDPLFLSPKLIILANSVE-SSISEALCTG-IDP	813	PR	06-MAY-1999;	99US-0132486.
Db	891	NLAMILLDKDAWNKEEFSVLDELFTRSKVTFTRVPKIFLLATSATLTERSEMKSTGLIDE	950	PR	06-MAY-1999;	99US-0132487.
QY	814	PIVIVKPLRASMLAATLQRLGIGIREPPOHKGPPALILRNLLGRKILIVDDNNVNLRV	873	PR	07-MAY-1999;	99US-0132863.
Db	951	--VVIKPLRMSVLICCLQETLVNGKKRQPNRQ---RRNLGHLRLREKQILVVDDNLVNRV	1005	PR	11-MAY-1999;	99US-0132863.
QY	874	AAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMBMDGFEATRIRIRMEEMN	933	PR	14-MAY-1999;	99US-0134218.
Db	1006	AEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMBMDGFEATRIRVRELEREIN	1065	PR	14-MAY-1999;	99US-0134219.
QY	934	KRIKNGEALIVENGKNTSWHLPVLAMTADVIQATHEECLKCGMDGYVSKPFEAEQLYREV	993	PR	14-MAY-1999;	99US-0134221.
Db	1066	KKIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEEEVLYTAV	1125	PR	14-MAY-1999;	99US-0134370.
QY	994	SRFF 997		PR	18-MAY-1999;	99US-0134768.
Db	1126	ARFF 1129		PR	19-MAY-1999;	99US-0134941.
RESULT 6				PR	20-MAY-1999;	99US-0135124.
AAG47089				PR	21-MAY-1999;	99US-0135353.
XX	AAG47089 standard; Protein; 1176 AA.			PR	24-MAY-1999;	99US-0135629.
AC	AAG47089;			PR	25-MAY-1999;	99US-0136021.
XX	18-OCT-2000 (first entry)			PR	27-MAY-1999;	99US-0136392.
DT	Arabidopsis thaliana protein fragment SEQ ID NO: 59313.			PR	28-MAY-1999;	99US-0136782.
DE	Protein identification; signal transduction pathway; metabolic pathway;			PR	01-JUN-1999;	99US-0137222.
XX	hybridisation assay; genetic mapping; gene expression control; promoter;			PR	03-JUN-1999;	99US-0137528.
KW	termination sequence.			PR	04-JUN-1999;	99US-0137502.
XX	Arabidopsis thaliana.			PR	07-JUN-1999;	99US-0137724.
OS	EP1033405-A2.			PR	08-JUN-1999;	99US-0138094.
XX	06-SEP-2000.			PR	10-JUN-1999;	99US-0138540.
PN	25-FEB-2000; 2000EP-0301439.			PR	10-JUN-1999;	99US-0138847.
XX	25-FEB-1999; 99US-0121825.			PR	17-JUN-1999;	99US-0139492.
PR	05-MAR-1999; 99US-0123180.			PR	18-JUN-1999;	99US-0139454.
PR	09-MAR-1999; 99US-0123548.			PR	18-JUN-1999;	99US-0139455.
PR	23-MAR-1999; 99US-0125788.			PR	18-JUN-1999;	99US-0139456.
PR	25-MAR-1999; 99US-0126264.			PR	18-JUN-1999;	99US-0139457.
PR	29-MAR-1999; 99US-0126785.			PR	18-JUN-1999;	99US-0139458.
PR	01-APR-1999; 99US-0127462.			PR	18-JUN-1999;	99US-0139459.
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PR	23-MAR-1999; 99US-0125788.			PR	18-JUN-1999;	99US-0139750.
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PR	01-APR-1999; 99US-0127462.			PR	22-JUN-1999;	99US-0139899.
PR	06-APR-1999; 99US-0128234.			PR	23-JUN-1999;	99US-0140353.
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PR 26-AUG-1999; 99US-0150884.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 52.1%; Score 2685.5; DB 21; Length 1176;
Best Local Similarity 57.2%; Pred. No. 1.2e-222;
Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;

QY 61 WRK-LVVVVVFWVLVSIWTFWFSSQAMEKRKETLASMCDERARMLOQDFNVSMNHVQA 119
Db 230 WRKNILLGILGGVSFSVWFWFNDNEEIIIMKRRETLANMCDERARVLQDFNVSLNHVHA 289

QY 120 MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEREEFERQQGWT 179
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QY 180 IRKMYSLQNPVHKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVSLDMLSGKEDRENVL 239
Db 350 IKKMETEDQTVV--QDCVPENFDPAPIQDEYAPVIFAQETVSHIVSVDMMSGEEDRENIL 407

QY 240 RARSSGKGLTAPFPLIKTNRLGVILTFAYYKRDLPNATPKERIEATNGYLGGVFDIES 299
Db 408 RARASGKGLTSPFKLLKSNHLGVLTFAVYDTSLPDPATHEQRVEATIGYLGASYDMP 467

QY 300 LVENLLQOLASKQTI LVNVYDITNHSQPI SMYGTNV SADGLERVSPLIFGDP L RKHEMRC 359
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QY 360 RFKQKPPWPVLSMVTSGILVIALVAHIIHATVSRHKVEEDCDKMKQLKKAEAAADVA 419
Db 528 RFKHKLPWPWTAITPSILVLVITFLVGYILYEA INRIATVEEDCQKMRELKARAEADIA 587

QY 420 KSQFLATVSHEIRTPMNGVLGMLHMLMDTDLDTQDYVTAQASGKALVSLINEVL DQA 479
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QY 480 KTESGKLEEVRFDLRGILDVLSLFSSKQQKGYELAVYISDRVPDMLIGDPGRFRQI 539
Db 648 KIESGRLELENVPFDMRFILDNVSSLLSGKANEKIGIELAVYVSSQVPDVVVGDP SRFRQI 707

QY 540 LTNLMGNSIKFT-EKGHIFVTVHLVDEL FESIDGETA-----SSPESILSGLPVA 588
Db 708 ITNLVGN SIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSESETVSGFP 767

QY 589 DRQRSWENFK-AFSSNGHRSEFPSPDPDINLIVSVEDTGVGIPVEAQSRIFTPFMQVGP SI 647
Db 768 NAWGSKNFKTCYSTESQNS-----DQIKLLVTVEDFGVGPVDAQGRIFTPFMQAD S 822

QY 648 SRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSFTFTTAVFSNGMQPAERKNDNNQPI 707

Db 823 SRTYGGTGIGLSISKRLVELMQGEMGFVSEPGIGSTFSTGTGVFG-----KAETNTSI 874

QY 708 -----FSEFRGMKAVVVDHRPARAKVSWYHFQRLGIRVEVVRVEQALHYLKIGTT 758

Db 875 TKLERFDLAIQEFGLRALVIDNRNIRAETRYELRRLGISADIVSSLRMACTCCISKLE 934

QY 759 TVNMILIEQEIWNREADDFIKKL---QKDPFLSPKLILLANSVE-SSISEALCTG-IDP 813

Db 935 NLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRVPKIFLLATSATLTERSEMKSTGLIDE 994

QY 814 PIVIVKPLRASMLAATLQRLGIGIREPPQHKGPPALILRNLLGRKILIVDDNNVNLRV 873

Db 995 --VVIKPLRMSVLICCLQETLVNGKKRQPNRQ--RRNLGHLRLREKQILVDDNLVNRV 1049

QY 874 AAGALKKYGADVCAESGIIKAIISLLKPPHEFDACFMDIQPMDGFEATRIRIRDMEEEMN 933

Db 1050 AEGALKKYGAIVTCVESGKAALAMLKPPHNFDAFMDLQMPMDGFEATRIRVRELEREIN 1109

QY 934 KRIKNGEALIVENGKTSWHLPLVLAAMTADVIQATHEBCLKCGMDGYVSKPFEAEQLYREV 993

Db 1110 KXIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEBCKMCGMDGYVSKPFEDEVLYTAV 1169

QY 994 SRRF 997

Db 1170 ARPF 1173

RESULT 7

ABG70781

ID ABG70781 standard; Protein; 1176 AA.

XX

AC ABG70781;

XX

DT 09-DEC-2002 (first entry)

XX

DE A. thaliana cytokinin receptor, AHK2, protein.

XX

KW AHK2; plant; antagonist; agonist; cytokinin receptor;

KW receptor; signal transduction; histidine kinase; hormone; cell division;

XX cell differentiation; agriculture; growth regulator; harvest.

OS Arabidopsis thaliana.

FH Key Location/Qualifiers

FT Region 50..1176

FT /note= "This region is specifically claimed in Claim 1"

FT Region 196..1176

FT /note= "This region is specifically claimed in Claim 1"

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PN EPI241182-A2.

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PD 18-SEP-2002.

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PF 13-MAR-2002; 2002EP-0005749.

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PR 15-MAR-2001; 2001JP-0073812.

PR 29-JUN-2001; 2001JP-0198639.

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PR 29-JUN-2001; 2001JP-0198640.

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PA (SUMO) SUMITOMO CHEM CO LTD.

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PI Kakimoto T, Higuchi M, Inoue T;

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DR WPI; 2002-693041/75.

DR N-PSDB; ABS54450.

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PT Analyzing agonist or antagonist activity of a substance for use as a

PT plant growth regulator, comprises measuring intracellular signal

PT transduction from a cytokinin receptor expressed in a cell contacted

PT with the test substance -

XX

XX

PS Claim 1; Page 26-28; 47pp; English.

XX

CC The invention discloses a method for analysing antagonist or agonist

CC activity to a cytokinin receptor. The method comprises bringing a

CC candidate substance into contact with a transformed cell, in which a DNA

CC encoding the receptor has been introduced, and then measuring the

CC existence, or the quantity, of the intracellular signal transduction from

CC the receptor expressed in the cell. The cytokinin receptor comprises an

CC extracellular region of the receptor, transmembrane regions, a histidine

CC kinase region and a receiver region of the kinase. The transmembrane

CC regions and kinase region are homogeneous to each other and the receptor

CC region is heterogeneous to them. Cytokinins are plant hormones relevant

CC to cell division and differentiation of higher plants. The method is used

CC for analysing agonist or antagonist activity to a cytokine receptor. A

CC substance with agonist or antagonist activity to the receptor can be

CC used, in agriculture, as a plant growth regulator, e.g. after harvest.

CC The advantage is that the candidate substances do not need to be prepared

CC in such large amounts as in previous methods and that the method avoids

CC the immensely long time to observe and evaluate the growth of the plant

CC and the physiological changes of the plant after spraying. The sequence

CC presented is the A. thaliana cytokinin receptor, AHK2, protein.

XX

SQ Sequence 1176 AA;

Query Match 52.1%; Score 2685.5; DB 23; Length 1176;

Best Local Similarity 57.2%; Pred. No. 1.2e-222;

Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;

QY 61 WRK-LVVVVVFWVLVSIWTFWYFSSQAMEKKKETLASMCDERARMLQDNVSMNHVQA 119

Db 230 WRKNILLGILGGVSFVWFWDTNEEIIKKRETLANMCDERARVLQDNVSLNHVHA 289

QY 120 MSILISTFHHGKIPSAIDQRTFSEYTDRTSPERPLTSGVAYAMRVLHSEEEFERQQCWT 179

Db 290 LsILVSTFHHGKIPSAIDQRTFEEYTERINFERPLTSGVAYALKVPHSREKFEKEHGA 349

QY 180 IRKMSYLEQNPVHKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVL 239

Db 350 IKKMETEDQTVV--QDCVPENFDPAPIQDEYAPVIFAQETVSHIVSDMMSGEEDRENIL 407

QY 240 RARSSGKGVLTAPFPLIKTNRLGVILTFVYKRDLPNSNATPKERIEATNGYLGVPFDIES 299

Db 408 RARASGKGVLTSPFKLLKSNHLGVLTFFAVYDTSLPPDATEEQRVEATIGYLGASDMP 467

QY 300 LVENLLQQLASKQTIILVNVDITNHSQIPISMYGTNVSADGLERSVPLIFGDPRLKHEMRC 359

Db 468 LVEKLLHQLASKQTIADVVDYDTNTSGLIKMYGSEIGDISEQHISSLDGDPSPRNHEMHC 527

QY 360 RFKQKPPWPVLSMVTSGILVIALLVAHITAHATVSRHKVEEDCDKMKQLKKAEEADVA 419

Db 528 RFKHKLPWPWTAITPSILVLVITFLVGYILYEAINRIATVEEDCCKMRELKARAEADIA 587

QY 420 KSQFLATVSHSHEIRTPMNGVLGMLHMLMDTDLVDTQDYVRTAQASGKALVSLINEVLDQA 479

Db 588 KSQFLATVSHSHEIRTPMNGVLGMLKMLMDTDLDAKQMDYAOQAHGSGKDLTSLINEVLDQA 647

QY 480 KIESGKLELEEVRFDLRGILDVLSLFSSKSQQKGVELAVYISDRVPDMLIGDPGRFRQI 539

Db 648 KIESGRLELENVPFDMRFILONVSSLLSGKANERKIELAVYSSQVDPDVVGDPSRFRQI 707

QY 540 LTNLMGNSIKFT-EKGHIFVTVHLVDELFESIDGETA-----SSPESTLSGLPVA 588

Db 708 ITNLVGNISIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSEGETVSGFPV 767

QY 589 DRQRSWENFK-AFSSNGHRSFEPSPPDINLIVSVEDTGVGIPVEAQSRIFTPFMQVGP 647

Db 768 NAWGSWKNFKTCYSTESQNS-----DQIKLLVTVEDTGVGIPVDAQGRIFTPFMQADSST 822

QY 648 SRTHGGTGIGLSISKLVGLMKGEIGFSSTPKVSGSTFTTFAVFSNGMQPAERKNDNNQPI 707

Db 823 SRTYGGTGIGLSISKRLVELMQGEMGFVSEPGIGSTFSTGTGVFG-----KAETNTSI 874

QY 708 -----FSEFRGMKAVVVDHRPARAKVSWYHFQRLGIRVEVVRVEQALHYLKIGTT 758

Db 875 TKLERFDLAIQEFGLRALVIDNRNIRAETRYELRRLGISADIVSSLRMACTCCISKLE 934

QY 994 SREF 997
Db 1170 ARFF 1173

RESULT 9
AAG47088
ID AAG47088 standard; Protein; 1238 AA.
XX
AC AAG47088;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 59312.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EF1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.

17-JUN-1999; 99US-0139492.
18-JUN-1999; 99US-0139454.
18-JUN-1999; 99US-0139455.
18-JUN-1999; 99US-0139456.
18-JUN-1999; 99US-0139457.
18-JUN-1999; 99US-0139458.
18-JUN-1999; 99US-0139459.
18-JUN-1999; 99US-0139460.
18-JUN-1999; 99US-0139461.
18-JUN-1999; 99US-0139462.
18-JUN-1999; 99US-0139463.
18-JUN-1999; 99US-0139750.
18-JUN-1999; 99US-0139763.
21-JUN-1999; 99US-0139817.
22-JUN-1999; 99US-0139899.
23-JUN-1999; 99US-0140353.
23-JUN-1999; 99US-0140354.
24-JUN-1999; 99US-0140695.
28-JUN-1999; 99US-0140823.
29-JUN-1999; 99US-0140991.
30-JUN-1999; 99US-0141287.
01-JUL-1999; 99US-0141842.
01-JUL-1999; 99US-0142154.
02-JUL-1999; 99US-0142055.
06-JUL-1999; 99US-0142390.
08-JUL-1999; 99US-0142803.
09-JUL-1999; 99US-0142920.
12-JUL-1999; 99US-0142977.
13-JUL-1999; 99US-0143542.
14-JUL-1999; 99US-0143624.
15-JUL-1999; 99US-0144005.
16-JUL-1999; 99US-0144085.
16-JUL-1999; 99US-0144086.
19-JUL-1999; 99US-0144325.
19-JUL-1999; 99US-0144331.
19-JUL-1999; 99US-0144332.
19-JUL-1999; 99US-0144333.
19-JUL-1999; 99US-0144334.
19-JUL-1999; 99US-0144335.
20-JUL-1999; 99US-0144352.
20-JUL-1999; 99US-0144632.
20-JUL-1999; 99US-0144884.
21-JUL-1999; 99US-0144814.
21-JUL-1999; 99US-0145086.
21-JUL-1999; 99US-0145088.
22-JUL-1999; 99US-0145085.
22-JUL-1999; 99US-0145087.
22-JUL-1999; 99US-0145089.
22-JUL-1999; 99US-0145192.
23-JUL-1999; 99US-0145145.
23-JUL-1999; 99US-0145218.
23-JUL-1999; 99US-0145224.
26-JUL-1999; 99US-0145276.
27-JUL-1999; 99US-0145913.
27-JUL-1999; 99US-0145918.
27-JUL-1999; 99US-0145919.
28-JUL-1999; 99US-0145951.
02-AUG-1999; 99US-0146386.
02-AUG-1999; 99US-0146388.
02-AUG-1999; 99US-0146389.
03-AUG-1999; 99US-0147038.
04-AUG-1999; 99US-0147204.
04-AUG-1999; 99US-0147302.
05-AUG-1999; 99US-0147192.
05-AUG-1999; 99US-0147260.
06-AUG-1999; 99US-0147303.
06-AUG-1999; 99US-0147416.
09-AUG-1999; 99US-0147493.
09-AUG-1999; 99US-0147935.
10-AUG-1999; 99US-0148171.
11-AUG-1999; 99US-0148319.
12-AUG-1999; 99US-0148341.
13-AUG-1999; 99US-0148565.

KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.

PN WO20024337-A2.

PD 06-JUN-2002.

PF 29-NOV-2001; 2001WO-US45053.

PR 29-NOV-2000; 2000US-253739P.

PA (UUNY) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.

PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;

PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants -

PS Example 1; Page 161-164; 187pp; English.

The invention relates to an isolated WOODEN LEG (WOL) polypeptide, comprising 15 contiguous amino acids of a fully defined Arabidopsis WOODEN LEG protein sequence of 1057 amino acids as given in the specification, and to its encoding nucleic acid. The invention also relates to an amino acid sequence of domains of protein, e.g., N-terminal region, C-terminal domain, etc; or is a naturally occurring allelic variant of the above mentioned polypeptide sequence. Expression levels of the nucleic acid can be modified to improve the vasculature in transgenic plants and enhance the agronomic properties of such plants. Also the WOL promoter is used to drive expression of a heterologous coding sequence of trees to improve wood production. The WOL nucleic acid may be used as a molecular marker for a qualitative trait loci, e.g., longer roots or enhanced wood production, in molecular breeding of crop plants. The nucleic acid is also useful in DNA amplification assays to identify the endogenous WOL genes, WOL mutant alleles and/or WOL expression products in cultivars as compared to wild-type plants. They can also be used as markers for linkage analysis of qualitative trait loci. The WOL protein and/or antibodies can be used as diagnostic reagents in immunoassays to detect expression of the WOL gene in cultivars and wild-type plants. The WOL protein, its encoding nucleic acid, and its corresponding antibody are useful for improving agronomically valuable plants e.g., trees. This sequence represents a protein relating to the wooden leg (WOL) protein of the invention.

Sequence	1173 AA;
----------	----------

Query Match	51.8%;	Score 2674;	DB 23;	Length 1173;
Best Local Similarity	57.0%;	Pred. No. 1.2e-221;		
Matches 549;	Conservative 142;	Mismatches 224;	Indels 48;	Gaps 13;

QY 61 WRK-LVVVWVFWVLVSIWTFWYFSSQAMEKRKETLASMCDERARMLQDQFNVSMMNHVOA 119

Db 230 WRKNILLGILGVSFVWFWDTNEEIIMKRRETLANMCDERARVLODQNVSLNHVHA 289

QY 120 MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEREEFERQQGWT 179

Db 290 LSILVSTFHHGKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSEREKFEKEHWA 349

QY 180 IRKMYSLQNPVHKDDYDLEALESPVQEEYAPVIFAQDTVSHVVS LDM LSGKEDRENVL 239

Db 350 IKKMETEDQTV--QDCVPENFDPAPIQDEYAPVIFAQETVSHIVSDMMSGEEDRENIL 407

QY	240	RARSSGKGVLTAPFPLIKTNRLGVILTFVAVYKRDLPSNATPKRIEATNGYLGVFDIES	299
		: : : : : : :	:
Dd	408	RARASCKGVLTSPFKLLKSNIHLGVLTFAVYDTSLPPDATEFORVEATIGVIGASYTMS	467

QY 300 LVENLLQLASKQTILVNVYDITNHSQPISMYGTNVSADGLERVSPLIFDPLRKHEMRC 359

Db 468 LVEKLLHOLASKOTIAVDYDTNTSGLIKMYGSEIGDISQHTSSIDECDPSNHEMVC 527

[illegible]

Qy	420	KSQFLATVSHEIRTPMNGVIGMLHMLMDTELDVTQQDYVRTAQSGKALVSLINEVLDOA	479
Db	588	KSQFLATVSHEIRTPMNGVIGMLHMLMDTDLDAKOMDYAOATAHGSGKDI.TSLINEVLDOA	647

Qy 480 KIESGKLEEEVRFDLRGILDDVLFLFSSKSQQKGVELAVYISDRVPDMLIGDPGRFRQI 539
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Dd 648 KIESGRLELENVPFDWRFILDNVSSLSGKANEKGLIAYVYSOVDVAWGDPSPRFRQI 707

QY	540	LTNLVGN SIKFT EKGHIF VTVHL VDLFE SIDGE TA----- SSPESTLS GLPVAD
db	708	ITNLVGN SIK--E RGHIFI SVHLA DEVKEP ITIEDAVI KOBLALG CSESCE TVCSCBAIM

[illegible]

QY	649	RTHGGTGIGLSISKCLVGLMKGEIGFSSSTPKVGSTFTTFAVSNGMQPAERKNDNNQPI -
	: :	-707
Db	821	RTYGGTGIGLSIKRLVEIMOGEMGFVSERPDISGSTSFGTCVGC-----KAEATNTGTF
	: :	-872

QY	708	-----FSEFRGMKAVVVDHRPARAKVSWYHFQRLGIRVEVVPRVEQALHYLKIGTTT	759
		: : : : : : : : : : :	
Db	873	KLERFDLAIQFTGLRALVIDNRNIRAETRVLYELRGISADIVSSIRMACTCCISKLEN	932

QY 760 VNMILIEQEIWNREADDFIKKL---QKDPLFLSPKLLILANSVE-SSISEALCTG-IDPP 814

Dd 933 LAMILIDKOAWNKEEFSVLDELFTRSKVTFETRPVKPIFIATSATI.TERSEMKSTGCIIDE- 901

Qy	815	IVIVKPLRASMLAATLQRLGIGIREPPQHKGP	PAIIIRNLILGRKILIVDDNNVLRVA	874
		: : :		
Dd	992	-WIKPLRMSVLICLQETLVNGKKQPNRQ---	ERNLGHLLREKOILVDDNIVNRVA	1047

QY	<div></div>	875 AGALKKYGADVVCASGIKAISLLKPPHEFDACFMDIQMPDMDGFETRIRDRMEEEMNK 934
Db	<div></div>	1048 EGALKKYGAIIVTCVESGKAALAMLKPPHNFDAFMLDPMPEDMGFEATRRVRERETNK 1107

QY	935	RKNGEALIVENGNTSWHLPLVLTAMTADVIQTAEHECLKCGMDGVSKPFEAEQLREVS	994
	:	:	:
	:	:	:
Dd	1108.	KIASGEVSAEMFCFSSWHVPILAMTADVIQTAEHECMKCGMDGVSKPFERRVYTAVA	1167

Qy 995 RFF 997

DB 1168 PFF 1170

RESULT 11
ABB93625
ID ABB93625 standard; Protein; 1173 AA.

AC ABB93625;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 2836.

KW Herbicidal; plant; agriculture; herbicide.

OS *Arabidopsis thaliana*.

PN WO200210210-A2.

CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
CC presented is the A. thaliana cytokinin receptor, CRE1, protein.
xx
SQ Sequence 1057 AA;

Query Match 48.1%; Score 2481.5; DB 23; Length 1057;
Best Local Similarity 50.9%; Pred. No. 4.6e-205;
Matches 536; Conservative 156; Mismatches 250; Indels 111; Gaps 18;

QY 21 MTTLLKKNKMWFWNKISSSGLKIPSPS-----YQFLGSKFKN----- 57
Db 43 LNSSEKPRKIDFWR---SGLM--GPAKMQQQOQLQHSVAVKMNNNNDLMGNKKGSTF 96

QY 58 ----KAWWRKLVVVVFWVLVSIWTFWYFSSQAMEKRKETLASCMDERARMLQDQNVVS 113
Db 97 IQEHRALLPKALILWIIIVGFISGIYQWMDANKIRREEVLVSMCDQRARMLQDQFSVS 156

QY 114 MNHVQAMSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEBEFE 173
Db 157 VNHVHALAILVSTFHYHKNPSAIDQETFAEYTARTAFERLLSGVAYAEKVNFEREMFE 216

QY 174 RQCGWTFIRKMYSLQNPVHKDDYDLAELPSPVQEEYAPVIFAQDTSVHVSLDMLSGKE 233
Db 217 RQHNWVIKTM-----DRGEPSVRDEYAPVIFSQDSVSYLESLDMMSGEE 261

QY 234 DRENVLRARSSGKGVLTAPFPLIKTNRLGVILTFVAVYKRLPSNATPKERIEATNGYLG 293
Db 262 DRENILRARETGKAVLTSPFRLETHHLGVLTFFPVYKSLPENPTVEERIAATAGYLG 321

QY 294 VFDEISLVENLLQOLASKQOTILVNVDITNHSQPISMYGT-NVSAD-GLERVSPLIFGDP 351
Db 322 AFDVESLVENLLGOLAGNQAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDFGDP 381

QY 352 LRKHEMRCRFKQKPPWPVLVSMVTSFGILVIALLVAHIIHATVSRHKEVEDCDKMKQLKK 411
Db 382 FRKHKMICRYHQKAPIPLNVLTVPLFFAIGFLVGYILYGAAMHIVKVEDDFHEMQELKV 441

QY 412 KAAEADVAKSQFLATVSHERTPMNGVLGMLMLMDTDLDTQDDYVRTAQASGKALVSL 471
Db 442 RAAEADVAKSQFLATVSHERTPMNGILGMLAMLDTLSTQDYAQTAQVCGKALIAL 501

QY 472 INEVLDOAKIESGKLEEEVRFDLRGILDVLSLFSSKSQKGVELAVYISDRVDPMLIG 531
Db 502 INEVLDRAKIEAGKLEESVFPDIRSILDVLSLFSESRNKGIELAVFVSDKVPEIVKG 561

QY 532 DPGRRFQILTNLMGNSIKFTTEKGHIFVTVHLVDELPESIDGETA-----SS 577
Db 562 DSGRRFQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQS 621

QY 578 PESTLSGLPVADRQRSWENKAFSSNGH--RSFEPSPDINLIVSVEDTGVGIPVEAQSR 635
Db 622 SYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDIS-SNVRLMVSIEDTGIGIPLVAQGR 680

QY 636 IFTPFMQVGPSISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTTAVFS---- 691
Db 681 VFMPFMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDK 740

QY 692 ----NGMQPAERKNDNNQPISEFRGMKAVVVDHRPARAKVSWYHFQRLGIRVEVVRVE 747
Db 741 CSAINHM-----KKPNVEHLPESTFKGMKAIVVDKAPVRAAVTRYHMKRLGINVDVVTSLK 795

QY 748 QAL----HYLKIGT-----TTVMILIEQEIW--NREADDFIKKIQK----DPLFLSPKL 792
Db 796 TAVVAAAAAFERNGSPLPTKPLQDMLVEKDSWISTEDNDSEIRLLNSRTNGNVHHSKSPKL 855

QY 793 ILLANSVESSISEALCTGIDPPPIVIVKPLRASMLAATLQRLGIGIGIREPPQHKGPPALIL 852
Db 856 ALPATNITNSEFDRAKSAGFADTVIMKPLRASMIGACIQQVLELRKTRQQHPEGSSPATL 915

QY 853 RNLLGRKILIVDDNNVNLRAAGALKKYGADVCAESGKAIKAILLKKPHEFDACFMDIQ 912
Db 916 KSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCABSGQVALGLLQIPHTFDACFMDIQ 975

QY 913 MPMDGFEATRRIRDMEEMNKRIKNGEALIVENGKNTSWHLPLVLTAMTADVIOATHEECL 972
Db 976 MPQMDGFEATRQIRMEKEAKEK-----TNLEWHLPILAMTADVIAHYEBCL 1023

QY 973 KCGMDGYVSKPFEAEQLYREVSRFFN-----SPS 1001
Db 1024 KSGMDGYVSKPFEENLYKSVAKSFKNPISPS 1056

RESULT 13
AAO22558
ID AAO22558 standard; Protein; 1057 AA.
XX
AC AAO22558;
XX
DT 28-OCT-2002 (first entry)
XX
DE Wooden leg (WOL) gene related protein SEQ ID No 5.
XX
KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.
XX
OS Arabidopsis thaliana.
XX
PN WO200244337-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US45053.
XX
PR 29-NOV-2000; 2000US-253739P.
XX
PA (UUNY) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.
XX
PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;
XX
DR WPI; 2002-599423/64.
XX
PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants -
XX
PS Claim 6; Fig 5D; 187pp; English.
XX
CC The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
CC comprising 15 contiguous amino acids of a fully defined Arabidopsis
CC WOODEN LEG protein sequence of 1057 amino acids as given in the
CC specification, and to its encoding nucleic acid. The invention also
CC relates to an amino acid sequence of domains of protein, e.g., N-terminal
CC region, C-terminal domain, etc; or is a naturally occurring allelic

variant of the above mentioned polypeptide sequence. Expression levels of the nucleic acid can be modified to improve the vasculature in transgenic plants and enhance the agronomic properties of such plants. Also the WOL promoter is used to drive expression of a heterologous coding sequence of trees to improve wood production. The WOL nucleic acid may be used as a molecular marker for a qualitative trait loci, e.g., longer roots or enhanced wood production, in molecular breeding of crop plants. The nucleic acid is also useful in DNA amplification assays to identify the endogenous WOL genes, WOL mutant alleles and/or WOL expression products in cultivars as compared to wild-type plants. They can also be used as markers for linkage analysis of qualitative trait loci. The WOL protein and/or antibodies can be used as diagnostic reagents in immunoassays to detect expression of the WOL gene in cultivars and wild-type plants. The WOL protein, its encoding nucleic acid, and its corresponding antibody are useful for improving agronomically valuable plants e.g., trees. This sequence represents a protein relating to the wooden leg (WOL) protein of the invention.

Query Match 48.0%; Score 2475.5; DB 23; Length 1057;
Best Local Similarity 50.8%; Pred. No. 1.5e-204;
Matches 535; Conservative 156; Mismatches 251; Indels 111; Gaps 18;

CC variant of the above mentioned polypeptide sequence. Expression levels of the nucleic acid can be modified to improve the vasculature in transgenic plants and enhance the agronomic properties of such plants. Also the WOL promoter is used to drive expression of a heterologous coding sequence of trees to improve wood production. The WOL nucleic acid may be used as a molecular marker for a qualitative trait loci, e.g., longer roots or enhanced wood production, in molecular breeding of crop plants. The nucleic acid is also useful in DNA amplification assays to identify the endogenous WOL genes, WOL mutant alleles and/or WOL expression products in cultivars as compared to wild-type plants. They can also be used as markers for linkage analysis of qualitative trait loci. The WOL protein and/or antibodies can be used as diagnostic reagents in immunoassays to detect expression of the WOL gene in cultivars and wild-type plants. The WOL protein, its encoding nucleic acid, and its corresponding antibody are useful for improving agronomically valuable plants e.g., trees. This sequence represents a protein relating to the wooden leg (WOL) protein of the invention.

QY 21 MTTLKKKNNKMFNWKISSGLKIPSPS-----YQFLGSKVFN----- 57
Db 43 LNSSEKPRKIDFWR---SGLM--GFAKMQQQQLQHSVAVKMNNNNNNDLGNKKGSTF 96
QY 58 ---KAWWRKLVVVVFWVLSIWTWFYFSSQAMEKREKTLASMCDERARMLQDQFNVS 113
Db 97 IQEHRALLPKALILWIIIVGFISSGIYQWMDANKIRREEVLSMCDQARMLQDQFSVS 156
QY 114 MNHVQAMSILISTFHGKIPSAIDQRTFSEYDRTSPERPLTSGVAYAMRVLHSEEEFE 173
Db 157 VNHVHALAILVSTFHYHKNPSAIDQRTFAEYRTARTAPERLLSGVAYAEKVYVNEREMFE 216
QY 174 RQGWTRKMYSLQNPVHKDDYDLEALEPSVQEEYAPVIFAQDVTSHVVSLLDMLSGKE 233
Db 217 RQHNWIKTM-----DRGEPSVRDEYAPVIFSQDSVSYLESILDMMSGEE 261
QY 234 DRENVLARSSGKGLTAPPLIKTNRLGVILTFAYVKRDLPSNATPKERIEATNGYLG 293
Db 262 DRENILARETGKAVLTSPFRLLETHLGVLTFFPVYKSSLPENPTVEERIAATAGYLG 321
QY 294 VFDIESLVENLLQQLASKQTLVNVYDITNHSQIPSMYGT-NVSAD-GLERSVPLIFGDP 351
Db 322 AFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDGDP 381
QY 352 LRKHMRCPKQKPPWPVLSMTVSFGLVIALVIAHIIHATVSRHKVEEDCKMKQLKK 411
Db 382 FRKHKMICRYHOKAPIPLNVLTFPLFAIGFLVGYLYGAAMHIVKVEDDFHEMQELKV 441
QY 412 KAEAAADVAKSQFLATVSHEIRTPMNGVLMHMLMDTDLVTDQDYVVRTAQASGKALVSL 471
Db 442 RAEAAADVAKSQFLATVSHEIRTPMNGVLMHMLMDTDLVTDQDYVVRTAQASGKALIAL 501
QY 472 INEVLQAKIESGKLEEVRFDLRGILDDVLSLFSKSKQKGVELAVYISDRVPMILIG 531
Db 502 INEVLDRAKIEAGKLEESVFPDIRSILDDVLSLFSSESRNKSIELAVFVSDKVPFIVKG 561
QY 532 DPGFRFRQILTNLMGNSIKFTEKGHIFVTVHLVDELFSIDGETA-----SS 577
Db 562 DSGFRFRQIITNLVGNVSKFTEKGHIFVTVHLVDELFSIDGETA-----SS 577
QY 578 PESTLSGLPVADRQSRWENKAFSSNGH--RSFEPSPDINLIVSVEDTGVGIPVQAQSR 635
Db 622 SYNTLSGYEADGRNSWDSFKHLVSEQSLSSEFDIS-SNVRMLVSIEDTGIGIPVLAQQR 680
QY 636 IFTPFMVGPSISRTHGGTGIGLSISKLVGLMKGEIGFSSFPKVGSTFTTFAVFS---- 691
Db 681 VFMPFMQADSSTSRNYGGTGIGLSISKLVGLMRGQINFISRHIGSTFTTFAVLEKCDK 740
QY 692 ---NGMQPAERKNDNNQPIFSEFRGMKAVVVDHRPARAKVSWHFORLIRVEVVRVE 747

Db 741 CSAINHM-----KXPNVEHLPSFTFGKMAIVVDKAPVRAAVTRYHMKRLGINVDVVTSLK 795
QY 748 QAL-----HYLKIGT-----TTVMILIEQBIW--NREADDFFIKKLOK-----DPLFLSPKL 792
Db 796 TAVVAAAFAFERNGSPLPKQPLDMILVEKDSWISTEDNDSEIRLLNSRTNGNVHHSKPKL 855
QY 793 ILLANSVSESSISEALCTGIDPPVIVVPLRASMLAATLQRLGIGIGIREPPQHKGPALIL 852
Db 856 ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLOQVLELRKTRQOHPEGSSPATL 915
QY 853 RNLLGRKILIVDDNNVNLRAAGALKKYGADVVCAESGIIKAIISLLKPPHEFDACFMDIQ 912
Db 916 KSLLTGKKILVVDNIVNRRVAAGALKKFGAEVVCVCAESGQVAGLGLQIPHTFDACFMDIQ 975
QY 913 MPMDGFEATRRIRDMEEEMNKRIKNGEALIVENGKNTSWHLPLVAMTADVIOATHEECL 972
Db 976 MPQMDGFEATRQIRMEKETKEK-----TNLEWHLPLAMTADVVIHATYEEL 1023
QY 973 KCGMDGYVSKPFEAEQLYREVSRFFN-----SPS 1001
Db 1024 KSGMDGYVSKPFEENLYKSVAKSFKNPISPS 1056

RESULT 14
AAO22570
ID AAO22570 standard; Protein; 1057 AA.
XX
AC AAO22570;
XX
DT 28-OCT-2002 (first entry)
XX
DE Wooden leg (WOL) gene related protein SEQ ID No 24.
XX
KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.
XX
OS Arabidopsis thaliana.
XX
PN WO200244337-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US45053.
XX
PR 29-NOV-2000; 2000US-253739P.
XX
PA (UINY) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.
XX
PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M; Benfey PN;
XX
WPI; 2002-599423/64.
XX
PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set of asymmetric cell divisions that establish vascular tissue in root and hypocotyl development, useful for improving agronomically valuable plants -
XX
PS Disclosure; Page 167-171; 187pp; English.

XX
CC The invention relates to an isolated WOODEN LEG (WOL) polypeptide, comprising 15 contiguous amino acids of a fully defined Arabidopsis WOODEN LEG protein sequence of 1057 amino acids as given in the CC specification, and to its encoding nucleic acid. The invention also CC relates to an amino acid sequence of domains of protein, e.g., N-terminal CC region, C-terminal domain, etc; or is a naturally occurring allelic CC variant of the above mentioned polypeptide sequence. Expression levels of

CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of
CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.

SQ Sequence 1057 AA;

Query Match 48.0%; Score 2475.5; DB 23; Length 1057;
Best Local Similarity 50.8%; Pred. No. 1.5e-204;
Matches 535; Conservative 156; Mismatches 251; Indels 111; Gaps 18;

QY 21 MTTLKKKMKWFWNKKISSGLKIPFS-----YQLGSKVKN----- 57
DB 43 LNSSEPRKIDFWR---SGLM--GPAKMQQQQLQHSVAVKMNNDLNGNKKGSTF 96
QY 58 ----KAWWRKLVVVVFWVWVLSIWTFWYFSSQAMEKREKTLASCMDEARMLQDFNVS 113
DB 97 IQEHRALLPKALILWIIIVGFISSGIYQWMDANKIRREEVLSVSMCDQARMLQDFSVS 156
QY 114 MNHVQAMSLISTFHGKIPSAIDQRTSEYTDRTSPERLTSGVAYAMRVLSHREEF 173
DB 157 VNHVHALILVSTFHYHKNPSAIDQRTFAETARTAFERLLSGVAYAEKVNVFEREMFE 216
QY 174 RQGWTRKMYSLQNPVHKDDYDLEALBPSPVQEEYAPVIFAQDVTSHVVSLSLMSGKE 233
DB 217 RQHNWVITM-----DRGEPSVRDEYAPVIFSQDSVSYLESLDMMSGEE 261
QY 234 DRENVLARSSGKGLVTAFFPLIKTNRLGVILTAFAVKRDLPSNATPKERIEATNGYLG 293
DB 262 DRENILRARETGKAVLTSPFRLLHHLGWLTTPVYKSLPENPTVEERIAATAGYLG 321
QY 294 VFDIESLVENLLQQLASKQTLVNVYDITNHSQPISMYGT-NVSAD-GLERSVPLIFGDP 351
DB 322 AFDVESLVENLLQQLAGNAIVVHVYDITNASDPLVMYGNQDEADRSLSHESKLDGDP 381
QY 352 LRKHEMRCKFKQPPVPLSVMTSFGILVIALVAHIIHAFVSRHKEVEDCDKMKQLKK 411
DB 382 FRKHMKICRYHQKAPILNVLTTVPLFFAIGLVGYIYGAAMHIVKVEDDFHEMQELKV 441
QY 412 KAEAADVAKSQFLATVSHVIRTPMNGVGLMHLMDTDLTQDQVVRTAQASGKALVSL 471
DB 442 RAEAADVAKSQFLATVSHVIRTPMNGVGLMHLMDTDLTQDQVVRTAQASGKALVSL 501
QY 472 INEVLDAQIESGKLEEVRFDLRGILDDVLSFSSKSOQKGVAVYISDRVPDMLIG 531
DB 502 INEVLDRAKIEAGKLEESVPFDIRSILDDVLSFSESRNKSIELAVFVSDKVPEIVKG 561
QY 532 DPGFRFQILTMGNISIKFTEKGHIFVTVHVLVDELFESEIDGETA-----SS 577
DB 562 DSGFRFQIILNVGNSVKFTEKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVSKQS 621
QY 578 PESTLSGLPVADRQSRWENFKAFSSNGH--RSFEPSPDDINLVSVEDTGVGIPVEAQSR 635
DB 622 SYNTLSGYEADGRNSWDSFKHLVSEBQSLSEFDDIS-SNVRMLVSIEDTGIGIPLVAQGR 680
QY 636 IFTPFMQVGPSISRTHGGTGIGLSISKCLVGLMKGEIGFSPTPKVSGSTFTTAVFS---- 691
DB 681 VFMFPMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFISRHIGSTFWTAVLEKCDK 740
QY 692 ----NGMQPAERKNDNNQPIFSEFRGMKAVVVDHRRPARAKVSWYHFQRLGIRVEVPRVE 747

DB 741 CSAINHM-----KKPNVEHLPSTFKGMKAIIVDAKPVRAAATRYHMKRLGINVDVVTSLK 795
QY 748 QAL-----HYLKIGT-----TTVMILIEQEIW--NREADDFIKKLQK----DPLFLSPKL 792
DB 796 TAVVAAAFAFRNGSPLPKQDMLILVEKDSWISTEDNDSEIRLLNSRTNGNVHKKSPKL 855
QY 793 ILLANSVSEISALCTGIDPPIVIVKPLRASMLAATLQRLGIGIREPPQHKGPALIL 852
DB 856 ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQVLELRKTRQOHPEGSSPATL 915
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DB 916 KSLTGKILVDDNIVNRRVAAGALKKFGAEVCAESGQVALGLLQIPHTFDACFMDIQ 975
QY 913 MPEMDGFEATRIRDMEEEMNKIKNGEALIVENGKNTSWHLPLVLAAMTADVIQATHEECL 972
DB 976 MPQMDGFEATRIRDMEEEMNKIKNGEALIVENGKNTSWHLPLVLAAMTADVIQATHEECL 1023
QY 973 KCGMDGVSKPFEAEQLYREVSREFN---SPS 1001
DB 1024 KSGMDGVSKPFEAEQLYREVSREFN---SPS 1056
RESULT 15
AAE33694
ID AAE33694 standard; Protein; 1057 AA.
XX
AC AAE33694;
XX
DT 16-APR-2003 (first entry)
XX
DE Arabidopsis thaliana histidine kinase 4 (AHK4)-WOL, CRE1 protein.
XX
KW Shoot formation; senescence; transgenic; transgenic plant; agriculture;
KW cell proliferation; shoot meristem formation; leaf development; AHK;
KW photosynthesis; histidine kinase; enzyme; CRE1.
XX
OS Chimeric - Arabidopsis thaliana.
OS Chimeric - Unidentified.
XX
PN WO200299079-A2.
XX
PD 12-DEC-2002.
XX
PF 06-JUN-2002; 2002WO-US18066.
XX
PR 06-JUN-2001; 2001US-296554P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PI Sheen J, Hwang I;
XX
DR WPI; 2003-140613/13.
XX
PT Increasing yield in plant, increasing shoot formation in a plant, or
PT delaying senescence in a plant such as wheat, rice, maize, barley,
PT potato, by using transgenes that regulate cytokinin response -
XX
PS Disclosure; Page 80-82; 87pp; English.
XX
CC The present invention relates to a novel method of increasing yield in a
CC plant, increasing shoot formation or delaying senescence in a plant. The
CC method involves introducing into plant cells, a transgene having a B-type
CC response regulator operably linked to a promoter functional in plant
CC cells to yield transformed plant cells or whose expression reduces the
CC expression of A-type response regulator in the cells of the plant and
CC regenerating a plant from the transformed cells. The method is useful
CC for increasing the yield in a plant, increasing the shoot formation or
CC delaying senescence in a plant such as wheat, rice, maize, barley,
CC potato, tomato, soybean, tomato, oat, cotton and sunflower. The method
CC is useful for variety of agricultural and commercial purposes including
CC improving and enhancing photosynthesis, promoting cell proliferation,
CC shoot meristem formation, promoting leaf development, increasing crop

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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:02:30 ; Search time 27.0799 Seconds
(without alignments)
6681.678 Million cell updates/sec

Title: US-09-918-508-2_COPY_196_1176

Perfect score: 5019

Sequence: 1 KARGERKEKVLQALAPKK.....SKPFEEVLYTAVARFFPC 981

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 18443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	4991.5	99.5	1173	14	US-10-135-322-19
3	3291.5	65.6	1270	15	US-10-101-464A-979
4	2973.5	59.2	890	15	US-10-101-464A-958
5	2764	55.1	1002	15	US-10-101-464A-957
6	2685.5	53.5	1036	10	US-09-918-508-4
7	2651.5	52.8	1044	15	US-10-101-464A-956
8	2604	51.9	997	15	US-10-101-464A-977
9	2595.5	51.7	1092	14	US-10-135-322-18
10	2545.5	50.7	1057	10	US-09-918-508-6
11	2539.5	50.6	1057	14	US-10-135-322-5
12	2539.5	50.6	1057	14	US-10-135-322-24
13	2363	47.1	974	15	US-10-126-120-2
14	1378	27.5	480	15	US-10-101-464A-978
15	1132.5	22.6	426	15	US-10-101-464A-124

16	1063.5	21.2	482	15	US-10-101-464A-955	Sequence 955, Appl
17	1010.5	20.1	412	15	US-10-101-464A-905	Sequence 905, Appl
18	860	17.1	274	14	US-10-135-322-8	Sequence 8, Appl
19	844	16.8	289	14	US-10-135-322-10	Sequence 10, Appl
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21	642.5	12.8	2150	14	US-10-135-322-17	Sequence 17, Appl
22	594.5	11.8	1018	15	US-10-101-464A-909	Sequence 909, Appl
23	572.5	11.4	1829	15	US-10-156-761-10049	Sequence 10049, A
24	563.5	11.2	971	14	US-10-116-048-2	Sequence 2, Appl
25	563.5	11.2	2471	14	US-10-116-048-4	Sequence 4, Appl
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27	546	10.9	1447	15	US-10-156-761-8624	Sequence 8624, Ap
28	522	10.4	816	15	US-10-101-464A-827	Sequence 827, Appl
29	514	10.2	747	12	US-10-100-294A-27	Sequence 27, Appl
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31	487	9.7	1220	10	US-09-801-368-332	Sequence 332, Appl
32	478	9.5	1383	15	US-10-156-761-13096	Sequence 13096, A
33	462	9.2	185	15	US-10-101-464A-822	Sequence 822, Appl
34	455	9.1	123	14	US-10-135-322-12	Sequence 12, Appl
35	451.5	9.0	1373	12	US-10-032-585-7129	Sequence 7129, Ap
36	435.5	8.7	738	12	US-10-171-404A-36	Sequence 36, Appl
37	430.5	8.6	170	15	US-10-101-464A-116	Sequence 116, Appl
38	426	8.5	129	15	US-10-101-464A-828	Sequence 828, Appl
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41	414	8.2	100	14	US-10-135-322-29	Sequence 29, Appl
42	390	7.8	206	15	US-10-101-464A-120	Sequence 120, Appl
43	380.5	7.6	264	15	US-10-101-464A-959	Sequence 959, Appl
44	360.5	7.2	104	14	US-10-135-322-30	Sequence 30, Appl
45	357.5	7.1	773	12	US-10-171-404A-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-918-508-2
; Sequence 2, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1176
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-2

Query Match	100.0%	Score 5019;	DB 10;	Length 1176;
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QY 841 QILVVDNLVNRRAEGALKKYGAI VTCVESGKAALAMLPKPPHNFDA CFMDLQMPMDGF 900
Db 1036 QILVVDNLVNRRAEGALKKYGAI VTCVESGKAALAMLPKPPHNFDA CFMDLQMPMDGF 1095
QY 901 EATRRVRELEREINKKIASGEVSAEMFCKFSSWHVPILANTADVIOATHEECMKGMDGY 960
Db 1096 EATRRVRELEREINKKIASGEVSAEMFCKFSSWHVPILANTADVIOATHEECMKGMDGY 1155
QY 961 VSKPFEFEVLYTAVARFEPC 981
Db 1156 VSKPFEFEVLYTAVARFEPC 1176
```

RESULT 2

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US-10-135-322-19
; Sequence 19, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: "WOODEN LEG GENE, PROMOTER AND USES THEREOF"
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10135,322
; CURRENT FILING DATE: 2002-04-30
```

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; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1173
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-19
```

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Query Match 99.5%; Score 4991.5; DB 14; Length 1173;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 978; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KARGERKEKVHLQELALPKKQOQRAQTSSRGAGRWKRNILLGILGGVSFVWFWDTNE 60
Db 196 KARGERKEKVHLQELALPKKQOQRAQTSSRGAGRWKRNILLGILGGVSFVWFWDTNE 255
QY 61 EIMKRRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHHGKIPSAIDORTFEY 120
Db 256 EIMKRRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHHGKIPSAIDORTFEY 315
QY 121 ERTNFERPLTSGVAYALKVPHSREKFEKEHGWAIKMETEDQTVVQDCVPENPDPA 180
Db 316 ERTNFERPLTSGVAYALKVPHSREKFEKEHGWAIKMETEDQTVVQDCVPENPDPA 375
QY 181 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHGL 240
Db 376 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHGL 435
QY 241 AVYDTSPPDATEEQRVEATIGYLASDMPSPVLEKLLHQLASKQTIADVVDYDT 300
Db 436 AVYDTSPPDATEEQRVEATIGYLASDMPSPVLEKLLHQLASKQTIADVVDYDT 495
QY 301 IKMYGSEIGDISEQHISLDFGDPSPRNHEMCHRFKHLPIPWTAITPSILVLVIT 360
Db 496 IKMYGSEIGDISEQHISLDFGDPSPRNHEMCHRFKHLPIPWTAITPSILVLVIT 555
QY 361 ILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSHEIRTPMNGVL 420
Db 556 ILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSHEIRTPMNGVL 615
QY 421 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLLENVPEFDMRFLDN 480
Db 616 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLLENVPEFDMRFLDN 675
QY 481 GKANEKIGIELAVVSSQVDPVVGDPSPRFRQIITNLVNSIKFTQERGHIFIS 540
Db 676 GKANEKIGIELAVVSSQVDPVVGDPSPRFRQIITNLVNSIKFTQERGHIFIS 732
QY 541 KEPLTIEDAVLKORLALGCSSEGETVSGFPAVNAWGSKNFKTCYSTESQNSD 600
Db 733 KEPLTIEDAVLKORLALGCSSEGETVSGFPAVNAWGSKNFKTCYSTESQNSD 792
QY 601 VEDTGVGIPVDAQGRIFTFPMQADSSTSRTYGGTGIGLSISKRLVELMQGEM 660
Db 793 VEDTGVGIPVDAQGRIFTFPMQADSSTSRTYGGTGIGLSISKRLVELMQGEM 852
QY 661 GSTFSTGVFGKAEATNTSITKLERFDLAIQFTGLRALVIDNRNIRAEVTRV 720
Db 853 GSTFSTGVFGKAEATNTSITKLERFDLAIQFTGLRALVIDNRNIRAEVTRV 912
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFT 780
Db 913 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFT 972
QY 781 TSATLTERSEMKTGLIDEVVIKPLRMSVLI CCLQETLVNGKKRQPNRRNL 840
Db 973 TSATLTERSEMKTGLIDEVVIKPLRMSVLI CCLQETLVNGKKRQPNRRNL 1032
QY 841 QILVVDNLVNRRAEGALKKYGAI VTCVESGKAALAMLPKPPHNFDA CFMD 900
Db 1033 QILVVDNLVNRRAEGALKKYGAI VTCVESGKAALAMLPKPPHNFDA CFMD 1092
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Db 4 PSALDQKTFGEYTERTAERPLTSGVAYALKVPHSREQFEKRHDWTIKKMETADQTLVP 63

QY 168 DCVPENFDPAPIQDEYAPVIFAQETVSHIVSDMMSBEDRENILRARASGKGLTSPFK 227

Db 64 DYMLDRDPAPIQDEYAPVVFQETVSHIVSDMMSGEDRENILRARASGKGLTSPFK 123

QY 228 LKSNHGLGVLTFAVYDTSLPPDATEEQRVEATIGYGASDMPSLVEKLHLQASKQTI 287

Db 124 LKSNHGLGVLTFAVYDRELPAATAEQRIEATVYGASDVPVSLVEKLHLQASKQTI 183

QY 288 AVDYDTTNTSGLIKMYSBIDGISEQHISLSDFGDPSRNHEMHCRFKHKLPIPWTAITP 347

Db 184 VVNVDYDTNGSAPINMYGDDVIDTGLVRVSNVDFGDLRRHEMHCRFKQRPDPWTAINS 243

QY 348 SILVLVITFLVGYILYEAINRIATVEEDCQKMRRELKARAEAAADIAKSQFLATVSHEIRTP 407

Db 244 SVGLLVITLLVGHIFHAAINRIAKVEEDYRQMMELKSRAEAAADVAKSQFLATVSHEIRTP 303

QY 408 MNGVLGMLKMLMDTDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPPD 467

Db 304 MNGVLAMQLMLMDTNLANQLDYAQTAAHACGKDLISLINEVLDQAKIESGRLEKVPFD 363

QY 468 MRFILDNVSSLLSGKANEGIELAVYSSQVDPVVDGDPSPFRQIITNLVNSIKFTQER 527

Db 364 LRLALDNVLSIGRSNEKGIELAVYSDRPEAVIGDPGRFRQIITNLVNSIKFTHE- 422

QY 528 GHIFISVHLADEVKEPLTIEDAVLKQRLALGCSE- - - -SGETVSGFPAYNAWGSWNFK 582

Db 423 GHIFVSVHLEEGCSQHDFRD- -VEKRLSSNLVEDTSDKTFTNLGFGVQVDRRKSWERFK 480

QY 583 TCYSTESQNSDQI- - - -KLLVTVEDTGVGIPVDQAQGRIFTPFMQADSSTSRTYGGTGI 636

Db 481 - - - -KLNRSQDQDVNESVEVLVTVEDTGVGIAREAQSRIFTPFVQADSSTSRTYGGTGI 535

QY 637 GLSISKRLVELMQEMGFVSEPGIGSTFTSGVFGKAETNTSITKLERFDLAIQEFGLR 696

Db 536 GLSISKCLVDLMHGEIGFVSEPGTGSTFTSPFAKCEMNCLEVKQNYDSIISFRGLR 595

QY 697 ALVIDNRNIRAEVTRYELRLGISADIVSSLRMACTCCIS- - - -KLENLAMILIDKDAW 751

Db 596 ALVIDKRHRAEVARYHLERLRISVDVACSLKSACTYLSNSSPRELSDPDMVLIDKDVW 655

QY 752 NKE- - - -EFSVLDELFTRSKVTFTTRVPKIFLLATSATLTERSEMKSGLIDEVVIKPLR 806

Db 656 DRQTGLELNLISLWKHRQNSGVSIK- -PKIFLLATSISPIEHSSELKLANLVDNVLAKPLR 714

QY 807 MSVLICCLQETLVNGKKRQPNRQR- -RNLGHLHREKQILVDDNLVNRVVAEGALKKYGAI 865

Db 715 LSVLISFLQBALGNGKKRLSDRRKVSILGSLKGRILVDDNLVNRVVAEGALKKYGAI 774

QY 866 VTCVESGKAALAMLKPPHNFDA CFMDLQMPDMGFEATRVRRELEIREINKKIASGEVSAE 925

Db 775 VTCVSGKDAVAKLQPHDFAA CFMDLQMPDMGFEATRQIRHLESEVNSKIASGEVSSD 834

QY 926 MFECKFSSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEFEVLYTAVARFFE 979

Db 835 AFQNVVHHTPILAMTADVIQATNEECLKCGMDDYVSKPFEFEQLYSAVARFFE 888

RESULT 5

US-10-101-464A-957

; Sequence 957, Application US/10101464A

; Publication No. US20030046728A1

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Nicolaas

; APPLICANT: Higgins, Colleen M.

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

; FILE REFERENCE: 11000.1020c2

; CURRENT APPLICATION NUMBER: US/10/101,464A

; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: 09/704,302

; PRIOR FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: 09/228,986

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/162,866

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: PCT/US00/00724

; PRIOR FILING DATE: 2000-01-11

; NUMBER OF SEQ ID NOS: 989

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 957

; LENGTH: 1002

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

US-10-101-464A-957

Query Match 55.1%; Score 2764; DB 15; Length 1002;

Best Local Similarity 58.4%; Pred. No. 6.7e-245;

Matches 563; Conservative 140; Mismatches 223; Indels 38; Gaps 12;

QY 35 WRKNILLGILGGVSFVWFWDTNBEIIMKRRETLANCMCDERARVLQDQFNVLNHHVA 94

Db 47 WRK-LLXTWVFCATMFSLWIFSVMSSQAIEKRKETLASMCDERAQMLQDQFNVMNHHVQA 105

QY 95 LSILVSTFHHGKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSREKFEKEHGW 154

Db 106 MSILISTFHHGKSPSAIDQRTTFAEYTKRTAFERPLTSGVAYAVRVLHSEAEFEKQQGW 165

QY 155 IKKMETEDQTVV- -QDCVPENFDPAPIQDEYAPVIFAQETVSHIVSDMMSGEEDRENIL 212

Db 166 IQRMDTLEQNLVHKDDDFEVLPEPSPIQEYAPVIFAQDTVSHVSVSIDLLSGKEDRENVL 225

QY 213 RARASGKGLTSPFKLLKSNHGLGVLTFAVYDTSLPPDATEEQRVEATIGYGASDMP 272

Db 226 RARASGKGLTAPFRLLIKTNRLGVLTFAVYKTDLPNATPDERIQTATAGYIGIFHIQS 285

QY 273 LVEKLLHQLASKQTIADVVDYDTTNTSGLIKMYSBIDGISEQHISLSDFGDPSRNHEMH 332

Db 286 LVEKLLQQLASKQNLVNLVDITNQSHPISMYSGDEADDALEVSTLNFQDPFRKHEMRC 345

QY 333 RFKHLPIPWTAITPVSILVITFLVGYILYEAINRIATVEEDCQKMRRELKARAEAAADIA 392

Db 346 RFKQKPPWPWLAITTSYGLFVLAMLTGHICYATVNRIAKVEDDYQKMWELKKQAEAAADIA 405

QY 393 KSQFLATVSHEIRTPMNGVLGMLKMLMDTDLDAKQMDYAQTAHSGKDLTSLINEVLDQA 452

Db 406 KSQFLATVSHEIRTPMNGVLGMLHMLMHTDLDVTQDYVRTAQASGKALVSLINEVLDQA 465

QY 453 KIESGRLELENVPPDMRFLDNVSSLLSGKANEGIELAVYSSQVDPVVDGDPSPFRQI 512

Db 466 KIESGKLELEAVQFDLRAILDVLSLFSGKSQEKGVLELAFVIFSDQVPEKLIGDPGRFRQI 525

QY 513 ITNLVNSIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSESETVSGFP 572

Db 526 ITNLMGNSIKFT-EKGHIFVTVHQAQEVMSLDVETE- - - -SSSKNLTLSGFPVA 574

QY 573 NAWGSWKNFKT- - - -CYSTESQNSDQIKLLVTVEDTGVGIPVDAQGRIFTPFMQADS 625

Db 575 ERRLSWAKFKTFSQHERVC-SYPSSTYDLINLIVSVEDTGVGIPFEAQCRVTFPFMQVGP 633

QY 626 STSRTYGGTGIGLSISKRLVELMQEMGFVSEPGIGSTFTSGVFGKAETNTSITKLERF 685

Db 634 SISRTHGGTGIGLSISKRLVELMNGEVGVFSINVGSTFTTAVFNNGHNSNLNEYTCQQM 693

QY 686 - - -DLAIQEFGLRALVIDNRNIRAEVTRYELRLGISADIVSSLRMACTCCISKLENL 741

Db 694 NNQNSANSEFEFGMSALVDPDRSVRAKVSQYHVRQLGIQVEIVSDNLQVLSLKSRRPRI 753

QY 742 AMILIDKDAWKE-EFSVL- -DEL-FTRSKVTFTTRVPKIFLLATSATLTERSEMKSGLI 797

Db 754 DMVLIIEEVWNDSILFVDQLRHIDQKVT- - - -PRLFLAKSISSTRSDNVTCDTHS 809

QY 798 DEWIKPLRMSVLICCLQETLVN- - -GKKRQPNRQRNGLHLLREKQILVDDNLVNR 853

Db 810 PAVIMKPLRASMVAACLQRTMGNMKNKGNRYRNGEVSRSLQHLKILVDDNKVNLK 869
QY 854 VAEGALKYGAIVTCVSGKALAMLKPPHNFDA CFMDLQMPMDGF EATRVRVRELEREI 913
Db 870 VAAGALKRYGAELVCVSGKEAISLLTPPHSFYACFMDIQMPMDGF EATKTRDVEKSV 929
QY 914 NKKIAGBVSAAEMFCFSSWHVPIIANTADVIQATHEBCKMCGMDGYVSKPFEELVLYTA 973
Db 930 NRKIQLGEVSAEAGHGNVLNWHVPIIANTADVIHATQBECKMCGMDGYVSKPFEAQLYRE 989
QY 974 VARF 977
Db 990 VSRF 993
RESULT 6
US-09-918-508-4
; Sequence 4, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-4

Query Match 53.5%; Score 2685.5; DB 10; Length 1036;
Best Local Similarity 57.2%; Pred. No. 1.2e-237;
Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;
QY 35 WRKNILLGILGGVSFVSFWFWDNNEIIMKRRETLANMCDERARVLQDQFNVSINHVHA 94
Db 92 WRK-LVVVWVFWVLSIWFVSSQAMEKREKTLASCMCDERARMLQDQFNVSINHVQA 150
QY 95 LSLIVSTFHGKIPSAIDQRTFEETERTNFERPLTSGVAYALKVPHSREKEKEHGW 154
Db 151 MSILISTFHGKIPSAIDQRTFEETERTNFERPLTSGVAYAMRVLSHREKEKEHGW 210
QY 155 IKKMETEDQTVV--QDCVPENFDPAIQDEYAPVIFAQETVSHIVSDMMSGEEDRENIL 212
Db 211 IRKMYSLQNPVHKDDYDLEALFSPVQEEYAPVIFAQETVSHVSLDMLSGKEDRENVL 270
QY 213 RARASGKGLTSPFKLLKSNHGLGVLTFAVYDTSPPDATEEQRVEATIGYLGASVDMPS 272
Db 271 RARSSGKGLVTAPFPPLIKTNRLGVLTFAVYKRDLPNSATPKERIEATNGYLGVPDIES 330
QY 273 LVEKLLHQLASKQTIADVDTNTSGLIKMYGSEIGDISEQHISLDFGDPSPRNHEHC 332
Db 331 LVENLLQLASKQTIADVDTNTSGLIKMYGSEIGDISEQHISLDFGDPSPRNHEHC 390
QY 333 RPKHKLPIPWTAITPSILVLVITFLVGYLYEAINRIATVEEDCQKRELKARAEADIA 392
Db 391 RPKQKPPWPVLSMVTSGILVIALVAHIHATVSRHKVEEDCDKMKQLKKAADVA 450
QY 393 KSQFLATVSHETRTPMNGVGLMGLMLMDTDLDAKQMDYQAQTAHSGKDLTSLINEVLDOA 452
Db 451 KSQFLATVSHETRTPMNGVGLMGLMLMDTDLDAKQMDYQAQTAHSGKDLTSLINEVLDOA 510
QY 453 KIESGRLELENVFPDMRFILDNVSSLLSCKANEKGIELAVYSSQVVDVVGDPSPRFRQI 512

Db 511 KIESGKLEEEVFRDLRGILDDVLSLFSSKSQKGVELAVYISDRVPDMLIGDPGRFRQI 570
QY 513 ITNLVGNISIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSSEGTVSQFPVAV 572
Db 571 LTNLVGNISIKFT-EKGHIFVTVHLVDELFEIDGETA-----SSPESTLSGLPVA 619
QY 573 NAWGSKNFKTCYSTESQNS-----DQIKLLVTVEDTGVGIPVDAQGRIFTFEQADSSST 627
Db 620 DRQSRWENPK-AFSSNGHRSFEPSPDPDINLIVSVEDTGVGIPVEAQSRIFTFEQVGPSI 678
QY 628 SRTYGGTGIGLSISKRLVELMQGEMGFVSEPGIGSGTFSFTGVFG-----KAETNTSI 679
Db 679 SRTYGGTGIGLSISKRLVELMQGEMGFVSEPGIGSGTFSFTGVFG-----KAETNTSI 738
QY 680 TKLERPDLAIQEFGLRALVIDNRNIRAEVTRYELRLRGISADIVSSLRMACTCCISKLE 739
Db 739 -----FSEFRGMKAVVDHRRPARAKVSWYHFQRLGIRVEVPRVEQALHYLIKIGTT 789
QY 740 NLAMILIDKDAWNKEEFSVLDDELFTRSKVTFTTRVPKIFLLATSATLTERSEMKTGLIDE 799
Db 790 TVNMILIEQEIWNREADDFIKKL--QKDPFLFLSPKILLANSVE-SSISEALCTG-IDP 844
QY 800 --VVIKPLRMSVLI CCLQETLVNGKKRQPNRQ---RRNLGHLRLREKQILVDDNVLNRRV 854
Db 845 PIVIVKPLRASMLAATLQRLGIGIGIREPPQHKGPPLILRLNLLGRKILVDDNVLNRRV 904
QY 855 AEGALKKYGAIVTCVSGKALAMLKPPHNFDA CFMDLQMPMDGF EATRVRVRELEREI 914
Db 905 AAGALKKYGADVCAESGKAIKSLKPPHNFDA CFMDLQMPMDGF EATRVRVRELEREI 964
QY 915 KKIASEVSAEMFCFSSWHVPIIANTADVIQATHEBCKMCGMDGYVSKPFEELVLYTA 974
Db 965 KRIKNGEALIVENGKNTSWHLPLVLA MTADVIQATHEBCKMCGMDGYVSKPFEELVLYTA 1024
QY 975 ARPF 978
Db 1025 SRFF 1028

RESULT 7
US-10-101-464A-956
; Sequence 956, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 956
; LENGTH: 1044
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-956

Query Match 52.8%; Score 2651.5; DB 15; Length 1044;
Best Local Similarity 54.8%; Pred. No. 1.7e-234;
Matches 549; Conservative 160; Mismatches 227; Indels 65; Gaps 17;
QY 9 KVLQALAPKKQQRAQTSSRGAGRWKRNILLGILGVSVFWFWDNNEIIMKRRE 68


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Db 65 KIH-----PSHNSQAGSKKFKRTWWRK-VLWTWIIIGWFIISACIPWYMSSQAAEKRRE 117
QY 69 TLANMCDERARVLQDQFNVLNHHVHALSILVSTFHHGKIPSAIDQRTFEEYTERTNFERP 128
Db 118 TLGSMCDERARMLQDQFNVMNHHVQAMSILSTFHHGKQPSAIDQRTFERYTERTAFERP 177
QY 129 LTSGVAYALKVPHSERKEFEKEHGWAIKKMETEDQTVV--QDCVPENFDPAPIQDEYAPV 186
Db 178 LTSFIAYAVRVLHCDREEFKAQGWKIKRMDTVEKTPVHKDNSELESESPVQEEYAPV 237
QY 187 IFAQETVSHIVSDMMSGEEDRENILRARASGKGLVTSPEFKLLKSNHGLGVLTFFAVYDTS 246
Db 238 IFAQDTIGHVVSLLDMLSGKEDRENVLRARASGKGLVTAPEFLIKTNSLGVILTFVAVYDKD 297
QY 247 LPPDATEEQRVEATIGYLGASYDMPSPVLEKLLHQLASKQTIADVVDYDTNTTSLGKIMYGS 306
Db 298 LPPNATPDERIEATDGYLGAFHIESLVEKLLQQLASKQNI VNVVYDTSNWSHPISMYGS 357
QY 307 EIGDISEQHISSLDFGDPSPRNHEMHCRFKHKLPIPWTAITPSILVLVITFLVGYILYEAI 366
Db 358 DVSEDYLEHVSTLNFEGDPFRKHEMRCRFRKQKSPWPWLAIITTSFGILVIALLVGYIFQATV 417
QY 367 NRIATVEEDCQKRELKARAEAAIAKSQPLATVSHEIRTPMNGVLGMLKMLMDTDLDAK 426
Db 418 NRIAKVEDDYHKMELKKAEEAADVAKSQPLATVSHEIRTPMNGVLGMLHMLMDTDLDET 477
QY 427 QMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFLDNVSSLLSGKANKEK 486
Db 478 QQDYVRTAQESKALVSLINEVLDQAKIESGKIEIEAVQFDLRAILDVLSLFSGKSQEK 537
QY 487 GIELAVYVSSQVDPVVVGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTI 546
Db 538 RVELAVYISENVPEKLIQDGPGRFRQIITNLMGNSIKFT-EKGHILVTVHLVDEV---MNS 593
QY 547 EDAVLKQRLALGCSESETVSGFPFPAVNAWGSWKNFKTCYSTE-----SQNSDQIKLV 599
Db 594 TDAEME-----SATRSTLSGFPVPDRRLSWAKFRT-FSQEGPASVPSPFSNPINLII 645
QY 600 TVEDTGVGIPVDAQGRIFTPFMQADSSRTYGGTGIGLSISKRLVELMQGEMGFVSEPG 659
Db 646 SVEDTGIGIPPEAQPRVFTRFMQVGPSTSRTHGGTGIGLSISKLVGLMNGEIGFVSIPQ 705
QY 660 IGSTFSFTGVFGKAEINTSITKLERF---DLAIQFTGLRALVIDNRNIRAEVTRYELR 715
Db 706 VGSTFTTAVFDDACSTSKCKGQQVKQGDSTSEFHGMKALVVDTRPVRANVSKYHIQ 765
QY 716 RLGISADIVSSLRMACTCCISKLEN---LAMILIDKDAWKEEFSVLDELFI-----TR 765
Db 766 RLGIHVEVVADLNQ---CLHTIQSGNCRIDMVLLWEIWDKD--SGLSAIFLDKLRDMK 819
QY 766 SKVTFTVRPKIFLLATSATLTERSEMKSSTGLIDEVVIKPLRMSVLICCLQETL----- 818
Db 820 PRVS----PRFLLSNSISSRMSGATDATGPFVIMKPLRASMLVASQFVGMGVNRI 875
QY 819 -VNGKKRQPNRQRNRLGHLLEKQILVVDDNLVNRRAEGALKKYGAIVTCVESGKAALA 877
Db 876 CSNGE--SPSLFLRN---LLRGRKILVVDDNKVNLRAEGALKKYGADVCTDSGEKALA 930
QY 878 MLKPPHNFDAFMDLQPEMDGFEATRRVRELEREINKKIASGEVSAEMFCKFSSWHVPI 937
Db 931 LLRPPHDFDAFMDIQMPGMDGFEATKRIRQMEQTPSKFEFLPGSSSEPRENISNFHLPI 990
QY 938 LAMTADVIQATHEECMKCGMDGYVSKPPEEEVLYTAVARFF 978
Db 991 LAMTADVIHATHEECTKYGMDGYVSKPFEAEQLFREVSRRFF 1031
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RESULT 8

US-10-101-464A-977
; Sequence 977, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:

```
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
; FILE REFERENCE: 11000.1020c2  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 977  
; LENGTH: 997  
; TYPE: PRT  
; ORGANISM: Eucalyptus grandis  
US-10-101-464A-977
```

Query Match 51.9%; Score 2604; DB 15; Length 997;
Best Local Similarity 54.1%; Pred. No. 3.6e-230;
Matches 547; Conservative 149; Mismatches 240; Indels 76; Gaps 15;

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QY 10 VHLQBALAPKKQQQAQTSRSGAGRWKRNILLGILGGVSPSVWFWDTNNEIIMKRRET 69
Db 14 VKLNEQVGTK---RGYTFIQSNRAWIPKILVLSVVGMAFLSMSIYRKMDADIKVRKEV 69
QY 70 LANMCDERARVLQDQFNVLNHHVHALSILVSTFHHGKIPSAIDQRTFEEYTERTNFERPL 129
Db 70 LVSMCDQARMLKDKQFSVSNHVHALAILVSTFHYKNPSAIDQETFAEYTARTAFERPL 129
QY 130 TSGVAYALKVPHSERKEFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQDEYAPVIFA 189
Db 130 LSGVAYAEVNTNSERKEFEHQGWITKMEKQ-----PSPVRDEYAPVIPS 175
QY 190 QETVSHIVSDMMSGEEDRENILRARASGKGLVTSPEFKLLKSNHGLGVLTFAVYDTSIPP 249
Db 176 QETVSYIESLDMMSGEEDRENILRARATGKAVLTSPFLLGSHHLGVLTFFPVYKSKLPP 235
QY 250 DATEEQRVEATIGYLGASYDMPSPVLEKLLHQLASKQTIADVVDYDTNTTSLGKIMYSEIG 309
Db 236 NPVVEERIEATVGYLGAFDVESLVENLLGQLDGNGAILNVYDVTNSSEPLIMYGHQYQ 295
QY 310 --DISEQHISSLDFGDPSPRNHEMHCRFKHKLPIPWTAITPSILVLVITFLVGYILYEAIN 367
Db 296 ECDTSLHESKLDGDPFRKHQMICRYHQKAPPSWTALTATFAFFVIGLLVGYILYGAAT 355
QY 368 RIATVEEDCQKRELKARAEAAIAKSQFLATVSHEIRTPMNGVLGMLKMLMDTDLDAKQ 427
Db 356 HIVKVEDDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLALLDTELSSTQ 415
QY 428 MDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFLDNVSSLLSGKANKEKG 487
Db 416 RBYAQTAQICGRKALIALINEVLDRAKIEAGKLELETVPFDIRSILDDVLSLFSSESRHKG 475
QY 488 IELAVYVSSQVDPVVVGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTI- 546
Db 476 IELAVFVADKVPEIVMGDPGRFRQIITNLVGNISIKFT-EKGHIFVKVHLADQVKGATNAH 534
QY 547 -----EDAVLKQRLALGCSESETVSGFPFPAVNAWGSWKNFKTCYS----- 586
Db 535 AKTCLNGRPEEDILISDSQL-----ETLSGCEVADERNSWDTFNLVVAEDQFNSVDSN 588
QY 587 -TESQNSDQIKLLVTVEDTGVGIPVDAQGRIFTPFMQADSSRTYGGTGIGLSISKRLV 645
Db 589 MTSNEASENVTVMVSVEDTGIGIPLRAQDRVFPMPQADSSRTYGGTGIGLSISKCLV 648
QY 646 ELMQGEMGFVSEPGIGSTFSFTGVFGKAEINTSITKLERFDLAIQFTGLRALVIDNRNI 705
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Db 649 ELMGCHINFISRPQIGSTESFTAVFGRCRLVFANVKRTFEDLPSPGFKGLKAIIVDGPV 708
Qy 706 RAEVTRYELRLGISADIVSSLRMACTCCISKLENLA-----MILIDXDAWNKEEFSV 758
Db 709 RAAVTRYHLNRLGINVEVASSIN-AITATGGKNGSLTAGYRHPDIIILVEKDMW---MSS 763
Qy 759 LDELET-----RSKVTFTRVPKIFLLATSATLTERSEMKSTGLIDEVVVTKPLRMSVLIC 812
Db 764 IDSWISLTADVADWKQNGNLIQLPKI-LLASKISASELEKAKASGFADTVIMKPVVRASMLAA 822
Qy 813 CLQETLVNGKKR--QPNRQRN----LGHLLREKQILVVDNLRNRRVAEGALKKYGAIV 866
Db 823 CLQOVLGIGRKKQLQKQDMNMRNGSSALRSLLYGKILVVDNKNVRRVAAGALKKFGANV 882
Qy 867 TCVESGKAALAMLKPPHNFDAFMDLQMPMDGFATRVRRELEREINKKIASGEVSAEM 926
Db 883 ECAESGKAALLELLQLPHDFDAFMDIQMPMDGFATRQIRLMESQVNEQMK--ESAVQ 940
Qy 927 FCKFSSWHVPILAMTADVIQATHEECMKCGMDGYVSKPPEEEVLYTAVARFF 978
Db 941 IVKGEWHMPILAMTADVIHATYDECLKCGMDGYVSKPPEDEENLYQAVAKFF 992

RESULT 9

US-10-135-322-18
; Sequence 18, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 18
; LENGTH: 1092
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-18

Query Match 51.7%; Score 2595.5; DB 14; Length 1092;
Best Local Similarity 55.0%; Pred. No. 2.6e-229;
Matches 538; Conservative 141; Mismatches 220; Indels 79; Gaps 14;
Qy 35 WRKNILLGILGVSVFWFWDNTEIIMKRRETLANCMDERARVLQDQFNVSINHVHA 94
Db 92 WRK-LVVVWVFWVLVSIWTFWYFSSQAMEKRKETLASCMCDERARMLQDQFNVSINHVQA 150
Qy 95 LSILVSTFHHGKIPSAIDQRTFEYTERTNFERPLTSGVAYALKVPHSREKFEKEHWA 154
Db 151 MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREFEERQGGWT 210
Qy 155 IKKMETEDQTVV--QDCVPENFDPAIQDEYAPVIFAQETVSHIVSVDMMSGEEDRENIL 212
Db 211 IRKMYSLQNPVHKDDYDLEALEPSVQEEYAPVIFAQTVSHVVSMDLSGKEDRENVL 270
Qy 213 RARASGKGLVTSPPFKLLKSNHLGVVLTFAVYDTSLPDPDATEEQRVEATIGYLGASVDMPS 272
Db 271 RARSSGKGLVTAFFPLIKTNRLGVILTFAVYKRDLPSPNATPKERIEATNGYLGGVFDIES 330
Qy 273 LVEKLLHQLASKQTIADVVDYDTNTSGLIKMYGSEIGDISQHISSLDGDPSPRNHEMH- 331
Db 331 LVENLLQLASKQTIILNVVDYDITNHSQFISMYGTNVSDAGLERSVSLIFGDPRLKHEMRC 390

Qy 332 -----CRFKHKLPIPWTAITPSILVLVITFLVGY 360
Db 391 RYLQLAHTYVNCFFLFARIQVLTFCCELLPLCRFKQKPPWPVLSMTVSGILVIALVAH 450
Qy 361 ILVEAINRIATVEEDCQKRELKARAEAAIAKQFLATVSHEIRTPMNGVGLMKMLMD 420
Db 451 ITHATVSRIHKVEEDCDKMKQLKKAAEAADVAKSQFLATVSHEIRTPMNGVGLMKMLMD 510
Qy 421 TDLDAKQMDYAQTAGSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFLDNVSSLLS 480
Db 511 TELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLELEEVRFDLRGILDDVLSLFS 570
Qy 481 GKANEKGIELAVVSSQVDPVVVGDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 571 SKSQKGVELAVYISDRVPDMLIGDPGRFRQILTNLMGNSIKFT-EKGHIFVTVHLVDEL 629
Qy 541 KEPLTIEDAVLKQRLALGCSSEGETVSGFPVAVNAWSWKFKTCYSTESQNS-----DQI 595
Db 630 FESIDGETA-----SSPESTLSGLPVADQRQSWENFK-AFSSNGHRSFEPSPPDI 678
Qy 596 KLLVTVEDTGVGIPVDAQGRIFTFPMQADSSTSYGGTGIGLSISKRLVELMQGEMGFV 655
Db 679 NLIVSVEDTGVGIPVEAQSRIFTFPMQVGPISIRTHGGTGIGLSISKRLVELMKGEIGFS 738
Qy 656 SEPGIGSTFSFTGVFG-----KAETNTSITKLERFDLAIQEFGLRALVIDNRNIRA 707
Db 739 STPKVGSTFTTAVFSNGMQPAERKNDNNQPI-----FSEFRGMKAVVVDHRRPARA 789
Qy 708 EVTRYELRRRLGISADIVSSLRMACTCCISKLENLAMILDKDANKKEEFSVLDDELFTRSK 767
Db 790 KVSWHFQRLGIRVEVVRVEQALHYLKIGTTTTVNMILLIEQIWNREADDFIKKL---QK 846
Qy 768 VTFTRVPKIFLLATSATLTERSEMKSTGLIDE--VVIKPLRMSVLICLQETLVNGKKRQ 825
Db 847 DPLFLSPKILLANSVE-SSISEALCTG-IDPPIVIVKPLRASMLAATLQRGDIGIREP 904
Qy 826 PNRQ--RRNLGHLLEKQILVVDNLRNRRVAEGALKKYGAIVTCVESGKAALAMLKPP 882
Db 905 PQHKGPPALILRNLLGRKILVDDNNVLRVAAAGALKKYGADVVCAESGKAIKLSLKPP 964
Qy 883 HNFDAFMDLQMPMDGFATRVRRELEREINKKIASGEVSAEMFCKFSSWHVPILAMTA 942
Db 965 HEFDACFMDIQMPMDGFATRIRDMEEEMNKRIKNGEALIVENGKNTSWHLFVLAMTA 1024
Qy 943 DVIQATHEECMKCGMDGY 960
Db 1025 DVIQATHEECLKCGMDGY 1042

RESULT 10

US-09-918-508-6
; Sequence 6, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-6
Query Match 50.7%; Score 2545.5; DB 10; Length 1057;

Best Local Similarity 53.3%; Pred. No. 9.9e-225;
Matches 538; Conservative 152; Mismatches 239; Indels 81; Gaps 17;

QY 4 GERKEKVLQE--ALAPKKQQQRAQTSSRGAGRWKNNILLGILGVSVFW-WFWDTNE 60
Db 89 GNKKGSTFIQEHRLLPKAL-----ILWIIIVGFSSGIYQWMDANK 131

QY 61 EIIMKRRETLANMCDERARVLQDFNVSLNHHVHALSILVSTFHHGKIPSAIDQRTFEY 120
Db 132 ---IRREEVLVSMCDQARMQLQDFSVSVNHVHALAILVSTFHHKNPASAIQETFAEY 188

QY 121 ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWALKMETEDQTVVQDCVPENFDPA 180
Db 189 ARTAFERPLLSSGVAYAEKVNFEREMFERQHNWIKTM-----DRGEPSVR 235

QY 181 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHGLVLT 240
Db 236 DEYAPVIFSQDSVSYLESMDMSGEEDRENILRARETGKAVLTSPFRLLETHHLGVLT 295

QY 241 AVYDTSLPDATEEQRVEATIGYLGASYDMPSELVVEKLLHQLASKQTIADVVDYDTNT 300
Db 296 PVYKSSLPENPTVEERIAATAGYLGAGFVDSLVENLLGQLAGNAQIAVVHVYDITN 355

QY 301 IKMYS--EIGDISEQHISLDFGDPSPRNHEMCHRFKHLPIPWTAITPSTILVITFL 358
Db 356 LVMYGNQDEEADRSLSHESKLDGDPFRKHMKICRYHOKAPIPLNVLTVPLFFAIGFL 415

QY 359 GYILYEAIRNATVEEDCQKRELKARAEADIAKSQFLATVSHEIRTPMNGVGLMKML 418
Db 416 GYILYGAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHEIRTPMNGILGML 475

QY 419 MDTDLDAKQMDYAOQTAHSGKDLTSLINEVLDQAKIESGRLELENVFPDMRFILDNV 478
Db 476 LDTELSSTQRTDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILD 535

QY 479 LSGKANEGIELAVYVSSQVDPVVGDPSPRNHEMCHRFKHLPIPWTAITPSTILVIT 538
Db 536 FSEESRNKGIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFT-EKGHIFVKV 594

QY 539 EVK---EPL-TIEDAVLKQRLALGCSEGETVSGPPAVNAWGSWKNFKTCYSTESQ 593
Db 595 QSKDESEPKNALNGVSEEMIVSVKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQ 654

QY 594 ----QIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSRTSYGGTGIGLSISKRL 649
Db 655 DISSNRLMVSIEDTGIGIPLVAQGRVFPMPQADSSRTSYGGTGIGLSISKCLVEL 714

QY 650 GEMGFVSEPGIGSTFSGTGFVFGKAEINTSITKLER--FDLAIQEFGLRALVIDNR 707
Db 715 GQINFISRHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPTSPFKGMKAIIVDAK 774

QY 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILDKDAW----- 753
Db 775 AVTRYHMKRLGINVDVWVTSKTAVVAAAFAERNGLPTKPKQLDMILVEKDSWIST 834

QY 754 EEFVLDLFTRSKVTFTVRPKIFLLATSATLTERSEMKSSTGLIDEVVIKPLRMSVL 813
Db 835 SEIRLNSR-TNGNV-HHKSPKALPATNITNSEFDRAKSAGFADTVIMKPLRASMIG 892

QY 814 LQETLVNGKKRQPNRQRN---LGHLLREKQILVDDNLVNRRAEGALKKYGAIVTC 870
Db 893 LQVLELRKTRQOHPEGSSPATLTKSLTGKILVDDNI VNRRAAGALKKFGAEVVC 952

QY 871 SGKAALAMLPKPPHNFACFMDLQMPMDGFEATRVRRELEREINKKIASGEVSAEM 930
Db 953 SGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQIRMEKEAKETN----- 1000

QY 931 SSWHPILAMTADVIQATHEECMKCGMDGVYVSKPFEFEVLYTAVARFFEP 980
Db 1001 LEWHLPIAMTADVIHATYEECLKSGMDGVYVSKPFEFEENLYSVAKSFKP 1050

RESULT 11

US-10-135-322-5
; Sequence 5, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-5

Query Match 50.6%; Score 2539.5; DB 14; Length 1057;
Best Local Similarity 53.2%; Pred. No. 3.5e-224;
Matches 537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;

QY 4 GERKEKVLQE--ALAPKKQQQRAQTSSRGAGRWKNNILLGILGVSVFW-WFWDTNE 60
Db 89 GNKKGSTFIQEHRLLPKAL-----ILWIIIVGFSSGIYQWMDANK 131

QY 61 EIIMKRRETLANMCDERARVLQDFNVSLNHHVHALSILVSTFHHGKIPSAIDQRTFEY 120
Db 132 ---IRREEVLVSMCDQARMQLQDFSVSVNHVHALAILVSTFHHKNPASAIQETFAEY 188

QY 121 ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWALKMETEDQTVVQDCVPENFDPA 180
Db 189 ARTAFERPLLSSGVAYAEKVNFEREMFERQHNWIKTM-----DRGEPSVR 235

QY 181 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHGLVLT 240
Db 236 DEYAPVIFSQDSVSYLESMDMSGEEDRENILRARETGKAVLTSPFRLLETHHLGVLT 295

QY 241 AVYDTSLPDATEEQRVEATIGYLGASYDMPSELVVEKLLHQLASKQTIADVVDYDTNT 300
Db 296 PVYKSSLPENPTVEERIAATAGYLGAGFVDSLVENLLGQLAGNAQIAVVHVYDITN 355

QY 301 IKMYS--EIGDISEQHISLDFGDPSPRNHEMCHRFKHLPIPWTAITPSTILVITFL 358
Db 356 LVMYGNQDEEADRSLSHESKLDGDPFRKHMKICRYHOKAPIPLNVLTVPLFFAIGFL 415

QY 359 GYILYEAIRNATVEEDCQKRELKARAEADIAKSQFLATVSHEIRTPMNGVGLMKML 418
Db 416 GYILYGAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHEIRTPMNGILGML 475

QY 419 MDTDLDAKQMDYAOQTAHSGKDLTSLINEVLDQAKIESGRLELENVFPDMRFILDNV 478
Db 476 LDTELSSTQRTDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILD 535

QY 479 LSGKANEGIELAVYVSSQVDPVVGDPSPRNHEMCHRFKHLPIPWTAITPSTILVIT 538
Db 536 FSEESRNKGIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFT-EKGHIFVKV 594

QY 539 EVK---EPL-TIEDAVLKQRLALGCSEGETVSGPPAVNAWGSWKNFKTCYSTESQ 593
Db 595 QSKDESEPKNALNGVSEEMIVSVKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQ 654

QY 594 ----QIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSRTSYGGTGIGLSISKRL 649
Db 655 DISSNRLMVSIEDTGIGIPLVAQGRVFPMPQADSSRTSYGGTGIGLSISKCLVEL 714

QY 650 GEMGFVSEPGIGSTFSGTGFVFGKAEINTSITKLER--FDLAIQEFGLRALVIDNR 707
Db 715 GQINFISRHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPTSPFKGMKAIIVDAK 774

QY 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILDKDAW----- 753
Db 775 AVTRYHMKRLGINVDVWVTSKTAVVAAAFAERNGLPTKPKQLDMILVEKDSWIST 834

QY 754 EEFVLDLFTRSKVTFTVRPKIFLLATSATLTERSEMKSSTGLIDEVVIKPLRMSVL 813
Db 835 SEIRLNSR-TNGNV-HHKSPKALPATNITNSEFDRAKSAGFADTVIMKPLRASMIG 892

QY 814 LQETLVNGKKRQPNRQRN---LGHLLREKQILVDDNLVNRRAEGALKKYGAIVTC 870
Db 893 LQVLELRKTRQOHPEGSSPATLTKSLTGKILVDDNI VNRRAAGALKKFGAEVVC 952

QY 871 SGKAALAMLPKPPHNFACFMDLQMPMDGFEATRVRRELEREINKKIASGEVSAEM 930
Db 953 SGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQIRMEKEAKETN----- 1000

QY 931 SSWHPILAMTADVIQATHEECMKCGMDGVYVSKPFEFEVLYTAVARFFEP 980
Db 1001 LEWHLPIAMTADVIHATYEECLKSGMDGVYVSKPFEFEENLYSVAKSFKP 1050

Db 715 GQINFISPHIGSTFWFTAVLEKCDKCSAINHMKKNVVEHLPSTFKGMKAIIVDAKPVRA 774
QY 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKDAW-----NK 753
Db 775 AVTRYHMKRLGINVDVTSKTAVVAAAFAFERNKSPKPLTKPQDMLIVKEDSWISTEDND 834
QY 754 EEFVLDLFTSRKVTFTVRPKLPLATSLTERSEMKSTGLIDEVVIKPLRMSVLICC 813
Db 835 SEIRLLNSR-TNGNV-HHKSPKALALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGAC 892
QY 814 LQETLVNCKKQPNRQRN---LGHLLEKQILVDDNLVNRRAEAGALKKYGAIVTCVE 870
Db 893 LQVLELRKTRQOHPEGSSPATLKSLLTGKILVDDNLVNRRAEAGALKKYGAIVTCVE 952
QY 871 SGKAALAMKPPHNFDAFMDLQMPMDGFEATRVRRELEREINKKIASGEVSAEMFCKF 930
Db 953 SGQVALGLLQIPHTFDACFMDIQMPMDGFEATRQIRMMKTKETKN-----1000
QY 931 SSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEFEVLYTAVARFFEP 980
Db 1001 LEWHLPIAMTADVIHATYEECLKSGMDGYVSKPFEFEENLYKSAKSKFP 1050

RESULT 12
US-10-135-322-24
; Sequence 24, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-24

Query Match 50.6%; Score 2539.5; DB 14; Length 1057;
Best Local Similarity 53.2%; Pred. No. 3.5e-224;
Matches 537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;
QY 4 GERKEVHLQE--ALAPKKQQQRAQTSSRGAGRWRKNILLGILGVSFVW-WFMDTNE 60
Db 89 GNKKGSTFIQEHRAALLPKAL-----ILWIIIVFISSGIYQWMDANK 131
QY 61 EIIMKRRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHHGKIPSAIDQRTFEYT 120
Db 132 ---IRREEVLVSMCDQARMLQDFSVSVNHVALAILVSTFHHKNPASIDQETPAEY 188
QY 121 ERTNFERPLTSGVAYALKVPHSERKEFEKHGWAIAKMETEDQTVVQDCVPENFDPAIQ 180
Db 189 ARTAFERPLLSGVAYAEKVVNFEREMFERQHNWIKTM-----DRGEPSVR 235
QY 181 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHLGVLTFF 240
Db 236 DEYAPVIFSQDSVSYLESMDMSGEEDRENILRARARETGKAVLTSPFRLLETHLGVLTFF 295
QY 241 AVYDTSLPDATEEQRVEATIGYLGASVDMPSLVEKLLHQLASKQTIADVDTNTSGL 300
Db 296 PVYKSSLPENPTVEERIAATAGYLGAFDVSILVENLLGLQAGNQAIVVHVYDITNASDP 355

QY 301 IKMYGS--BIGDISEQHISSLDGDPSPRNHEHMCREFKHLPIPWTAITPSILVLTFLV 358
Db 356 LVMYGNQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPILNVLTTVPLFFAIGFLV 415
QY 359 GYILYEAINRIATVEEDCOKKRELKARAAADIAKSQPLATVSHEIRTPMNGVLGMLKML 418
Db 416 GYILYGAAMHIVKVEDDFHEMOELKVRAEADVAKSQPLATVSHEIRTPMNGILGMLAML 475
QY 419 MDTLDLAKQMDYAQTAHGGKOLTSLINEVLDQAKIESGRLELENVFPDMRFLDNVSSL 478
Db 476 LDTELSSTQRDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPPDIRSILDDVLSL 535
QY 479 LSGKANEKIELAVYSSQVDPVVDPSRFRQIITNLVGNISIKFTQERGHIFISVHLAD 538
Db 536 FSESRNKSIELAVFVSDKVPBIVKSGDSGRFRQIITNLVGNISIKFT-EGHIFVKVHLAE 594
QY 539 EVK---EPL-TIEDAVLKQRLALGCSSEGETVSGFPVAVNAWGSWKNFKTCYSTESQNSD- 593
Db 595 QSKDESEPKNALNGGVSEEMIVVSKQSSYNTLSGYEADGRNSWDSFKHLVSEEQSLSEF 654
QY 594 ---QIKLLVTVEDTGVPDQAQGRIFTPEMQADSSSTRTYGGTGIGLSISKRLVEIMQ 649
Db 655 DISSNVRLMVSIEDTGIGIPVAQGRVFMFPMQADSSSTRTYGGTGIGLSISKRLVLMR 714
QY 650 GEMGFVSEPGIGSTFSTGTFGKAETNTSITKLER--FDLAIQEFGLRALVIDNRNIRA 707
Db 715 GQINFISPHIGSTFWFTAVLEKCDKCSAINHMKKNVVEHLPSTFKGMKAIIVDAKPVRA 774
QY 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKDAW-----NK 753
Db 775 AVTRYHMKRLGINVDVTSKTAVVAAAFAFERNKSPKPLTKPQDMLIVKEDSWISTEDND 834
QY 754 EEFVLDLFTSRKVTFTVRPKLPLATSLTERSEMKSTGLIDEVVIKPLRMSVLICC 813
Db 835 SEIRLLNSR-TNGNV-HHKSPKALALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGAC 892
QY 814 LQETLVNCKKQPNRQRN---LGHLLEKQILVDDNLVNRRAEAGALKKYGAIVTCVE 870
Db 893 LQVLELRKTRQOHPEGSSPATLKSLLTGKILVDDNLVNRRAEAGALKKYGAIVTCVE 952
QY 871 SGKAALAMKPPHNFDAFMDLQMPMDGFEATRVRRELEREINKKIASGEVSAEMFCKF 930
Db 953 SGQVALGLLQIPHTFDACFMDIQMPMDGFEATRQIRMMKTKETKN-----1000
QY 931 SSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEFEVLYTAVARFFEP 980
Db 1001 LEWHLPIAMTADVIHATYEECLKSGMDGYVSKPFEFEENLYKSAKSKFP 1050

RESULT 13
US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Sakakibara, Hitoshi
; APPLICANT: Takei, Kentaro
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FACTO
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match 47.1%; Score 2363; DB 15; Length 974;
Best Local Similarity 50.8%; Pred. No. 5.6e-208;
Matches 503; Conservative 152; Mismatches 251; Indels 84; Gaps 18;

QY 34 RWRKNILLG-ILGVSFVSFWFWDNTEELIMKRRETLANMCDERARVLQDQFNVLNVH 92
Db 12 RWRGLAAAGWVLTAVVCSAVMHWTLRRDSMDRAEERLVSMCEERARMLQEQFGVTNVHV 71
QY 93 HALSILVSTFHHGKIPSAIDQRTFEYTERTNFPERPLTSGVAYALKVPHSERKEFEKHG 152
Db 72 HAIAILISTFNEKSPPAIDQDTFAKYTARTSPERPLNGVAFQRPVPHHEREMFESQOG 131
QY 153 WAIKKNMETEDQTVVQDCVPENFDPAPIQDEYAPVIFAQETVSHIVSVDMMMSGEEDRENIL 212
Db 132 WVMNTMQRE-----PAPPQVEYAPVIFSQDVTVSYLARIDMMSGEEDRENIF 177
QY 213 RARASGKGVLTSPFKLLKSNHGLVWLTFAVYDTSPLPPDATEEQRVEATIGYLGAZYDMP 272
Db 178 RARTTGKAVLTNPFRLGSHLGNHGLVWLTFAVYRDPDLPADASVEQRTVEATIGYLGAFDVE 237
QY 273 LVEKLHLQASKQTIADVVDYDTNTSLGLIKMYSBIDISEQ---HISLDFDGPDSRNH 328
Db 238 LVENLLSKLAGNQDIVNVVYDVNTASDAMVLYGP--SSLDEQVPFLHVSMLDFGDPFRKH 295
QY 329 EMHCFPKHKLPIPTWTAITPSILVITFLVGYLYEAINRIATVEEDCQKRELKARAEA 388
Db 296 EMRCYRQKLPMPWSAITNPLGTFTVIWMLLGYSTAAAYSRYDKVTEDCRKEELKTOAEA 355
QY 389 ADIAKSOFLATVSHEIRTPMNGVLMKMLMDTDLDAKQMDYAOQTAHSGKDLTSLINEV 448
Db 356 ADVAKSOFLATASHEIRTPMNGVLMKMLMDTDLTWTQDYAOQTAQMCRALITLINDV 415
QY 449 LDOAKIESGRLELENVFPDMPFILDVSSLLSGKANEKIGIELAVYVSSQVDDVVGDPSR 508
Db 416 LDRAKIEAGKLELEAVPFDLRLSMDDDVSLFSSKSREKCIELAVFVCDNVPKVVIGDPWR 475
QY 509 FROITNLVGNISIKFTQERGHIPISVHLADEVKEPLTIEDAVLKORLALCSESSE- 564
Db 476 FROILTNLVGNVAVKFT-ERGHVFRVCLA-----ENSMNEANQVLHGAMNGKGRV 525
QY 565 -----TVSGFPAVNAWSGNKFKTCYS-----TESQN-----SDQIKLLVTVE 602
Db 526 ESTANGAFNTLSGFEEAADRNRNSQYFKLLLSKESLDDLESENQSDSDRVTLAISIE 585
QY 603 DTGVGIPVDAQRIFTPFMQADSSSTRTYGGTGIGLSIKRLVELMQGEMGFVSEPGIGS 662
Db 586 DTGVGIPVDAQDRVFTPFMQADSSSTRNYGGTGIGLSISKCLAEMLGGQISFTSHPSVGS 645
QY 663 TFSFTGVFGKAEATNTSITKLERFDLAI-QEFTGLRALVIDNRNIRAETVRYELRRLGISA 721
Db 646 TTFESATLKHSHKDIISGSSRSILTEALPTAFKGMKAILVDGRPVRSVAVTRYHLKRLGILL 705
QY 722 DIVSSLRMACTC-----CISKLENLAMILIDKDAWNKE-EFSVLDELFTRSKVTFTTRVP 774
Db 706 QVNNMNAVVKAFPGQNGAAGSREKASILFIESDFWRPETDVQLLNHLREQKNQGLSDGH 765
QY 775 KIFLLATSATLTERSEMSKSTGLIDEVVIKPLRMSVLICCLQETL-VNGKKRQPNRQRN- 832
Db 766 KVVLLVTS-----EADKDKYGSIFDIVMCKPIRASTIASIQQLLKVEIAERKDNQNRPSF 821
QY 833 LGHLLREKQILVDDNLVNRVRAEGALKKYGAIVTCVESGKAALAMLKPPHNFDAFMDL 892
Db 822 LRSLLVGNILVDDNKVNLVRAAALKKYGANVSCVESGKDAISLLQPPHREFACFMDV 881
QY 893 QMPMDGFEATRVRRELEREINK-----KIAS--GEVSAEMFCKFSSWHVPILANTADVIQ 946
Db 882 QMPMDGFEATGQIRQOMELKANEERKNKLASIEGSTTAE-----YHLPVLAMTADVIQ 934
QY 947 ATHEECMKCGMDGYVSKPFEEVLYTAVAR 976
Db 935 ATYEECIKSGMDGYVSKPFDEEQLYQAVSR 964

RESULT 14

US-10-101-464A-978

; Sequence 978, Application US/10101464A

; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 978
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-978

Query Match 27.5%; Score 1378; DB 15; Length 480;

Best Local Similarity 58.9%; Pred. No. 9.3e-118;

Matches 282; Conservative 67; Mismatches 110; Indels 20; Gaps 3;

QY 10 VHLQELALAPKQQQAQTSSRGAGRWKRNILLGILGVSVFWFWDNTEELIMKRRET 69
Db 14 VKLNEQVGTGK---RGYTFIQSNRAWIPKILVLVSVVGMAFLSMSIYRKMDADIKVRRKEV 69
QY 70 LANMCDERARVLQDQFNVLNVHVALSILVSTFHHGKIPSAIDQRTFEYTERTNFPL 129
Db 70 LVSMCDQARMLKDQFSVSNHVHALAILVSTFHHGKIPSAIDQRTFEYTERTNFPL 129
QY 130 TSGVAYALKVPHSERKEFEKHGWAIKKMETEDQTVVQDCVPENFDPAPIQDEYAPVIFA 189
Db 130 LSGVAYAEVNTSERKEFEKHGWTIKTMEKQ-----PSPVRDEYAPVIFS 175
QY 190 QETVSHIVSVDMMSGEDRENILRARASGKGVLTSPFKLLKSNHGLVWLTFAVYDTSLPP 249
Db 176 QETVSVIESLDMMSGEEDRENILRARATGKAVLTSPFRLGSHLGVLTFFPVYKSKLPP 235
QY 250 DATEEQRVEATIGYLGAZYDMPVSLVEKLLHQLASKQTIADVVDYDTNTSLGLIKMYGSEIG 309
Db 236 NPTVEERIEATVGYLGAFDVESLVENLLGQDGNQAILNVVDVNTSSEFLIMYGHQYQ 295
QY 310 --DISEQHISSLDGDPDSRNHEMHCRCFKHKLPIPTWTAITPSILVITFLVGYLYEAIN 367
Db 296 ECDTSLHESKLDGDPDFKHKQMICRYHQKAPPSWTALTATFAFFVIGLVGYLYGAAT 355
QY 368 RIATVEEDCQKRELKARAEAAADIAKSOFLATVSHEIRTPMNGVLMKMLMDTDLDAKQ 427
Db 356 HIVKVEDDFHEMQELKVRABEADVAKSQFLATVSHEIRTPMNGILGMLALLDTELSSTQ 415
QY 428 MDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVFPDMPFILDVSSLLSGKANEK 486
Db 416 RDAYAQTAICGKALIALINEVLDRAKIEAGKLELETVPFDIRSILDVLSLFSSESRHK 474

RESULT 15

US-10-101-464A-124

; Sequence 124, Application US/10101464A

; Publication No. US20030046728A1

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Nicolaas

; APPLICANT: Higgins, Colleen M.

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:54 ; Search time 32.8827 Seconds
(without alignments)
7698.569 Million cell updates/sec

Title: US-09-918-508-2_COPY_196_1176
Perfect score: 5019
Sequence: 1 KARGERKEKVHLQALAPKK.....SKPFEEVLYTAVARFFEP 981

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archheap:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5019	100.0	1176	10	Q9C5U2	Q9c5u2 arabidopsis
2	4991.5	99.5	1173	10	Q9FKH3	Q9fkh3 arabidopsis
3	3316	66.1	652	10	Q8GUG0	Q8gug0 arabidopsis
4	3297.5	65.7	1041	10	Q8L8I6	Q8l8i6 catharanthu
5	2685.5	53.5	1036	10	Q9C5U1	Q9c5u1 arabidopsis
6	2595.5	51.7	1092	10	Q9FZK3	Q9fzk3 arabidopsis
7	2575	51.3	1023	10	Q8RYG4	Q8ryg4 oryza sativ
8	2545.5	50.7	1057	10	Q9C5T9	Q9c5t9 arabidopsis
9	2545.5	50.7	1080	10	Q9C5T8	Q9c5t8 arabidopsis
10	2539.5	50.6	1057	10	Q9SIT0	Q9sit0 arabidopsis
11	2539.5	50.6	1080	10	Q9C5U0	Q9c5u0 arabidopsis
12	2520	50.2	925	10	Q8S6P5	Q8s6p5 oryza sativ
13	2363	47.1	974	10	Q9FRY7	Q9fry7 zea mays
14	1125	22.4	627	10	Q9AUQ0	Q9auq0 oryza sativ
15	791	15.8	1765	16	Q8EII0	Q8eii0 shewanella
16	786.5	15.7	1417	16	Q9HWR8	Q9hwr8 pseudomonas

17	784	15.6	1268	2	Q8KQV0	Q8kqv0 vibrio chol
18	782	15.6	2062	5	Q95PH6	Q95ph6 dictyosteli
19	778.5	15.5	1261	16	P73926	P73926 synechocyst
20	776	15.5	1331	16	Q9KSB0	Q9ksb0 vibrio chol
21	775	15.4	1320	16	Q8D5E0	Q8d5e0 vibrio vuln
22	765	15.2	1353	16	Q8DJE3	Q8dje3 synechococc
23	761	15.2	1299	16	Q8YUQ6	Q8yug6 anabaena sp
24	760	15.1	1364	16	Q8P883	Q8p883 xanthomonas
25	759.5	15.1	1364	16	Q8PJN8	Q8pjn8 xanthomonas
26	758	15.1	1550	16	Q8YQQ8	Q8yqq8 anabaena sp
27	756.5	15.1	1072	16	Q8D7S2	Q8d7s2 vibrio vuln
28	753.5	15.0	1462	16	P73035	P73035 synechocyst
29	751	15.0	928	16	Q8DC68	Q8dc68 vibrio vuln
30	743.5	14.8	1817	16	Q8YT51	Q8yt51 anabaena sp
31	740.5	14.8	1188	16	Q8EJ91	Q8ej91 shewanella
32	739	14.7	1000	17	Q8TPA1	Q8tpa1 methanosarc
33	731.5	14.6	1298	3	Q01318	Q01318 neurospora
34	731	14.6	1307	3	Q9C1U1	Q9clu1 magnaportha
35	725.5	14.5	786	16	Q98FG5	Q98fg5 rhizobium 1
36	725.5	14.5	1035	16	Q8DKI3	Q8dki3 synechococc
37	725	14.4	1243	16	Q8UCZ6	Q8ucz6 agrobacteri
38	723.5	14.4	1315	3	Q8X215	Q8x215 botrytis ci
39	723.5	14.4	1315	3	Q8X1E7	Q8x1e7 botrytis ci
40	721.5	14.4	801	3	Q9UUN8	Q9uun8 nectria hae
41	721.5	14.4	919	16	Q9HYE4	Q9hye4 pseudomonas
42	721	14.4	1283	3	Q94094	Q94094 nectria hae
43	720.5	14.4	1298	3	Q01309	Q01309 neurospora
44	717	14.3	935	16	Q8F370	Q8f370 leptospira
45	715	14.2	925	16	O31138	O31138 pseudomonas

ALIGNMENTS

RESULT 1

Q9C5U2

ID Q9C5U2 PRELIMINARY; PRT; 1176 AA.

AC Q9C5U2;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Histidine kinase.

GN AHK2.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21154803; PubMed=11230578;

RA Meguch C., Koizumi H., Suzuki T., Mizuno T.;

RT "Nevel family of sensor histidine kinase genes in Arabidopsis

RT Arabidopsis";

RL Plant Cell Physiol. 42:231-235 (2001)

DR EMBL; AB046869; BAB40774.1; -

DR HSSP; P06143; 1AB6.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; HSKA; 1.

DR Pfam; PF00072; response_reg; 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; HSKA; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW	Kinase; Phosphorylation; Sensory transduction.															
SQ	SEQUENCE 1176 AA; 131859 MW; AC0019CC612361BC CRC64;															
	Query Match 100.0%; Score 5019; DB 10; Length 1176;															
	Best Local Similarity 100.0%; Pred. No. 0;															
	Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;															
QY	1	KARGERKEKVHLQ	EALAPKQ	QOQRAQTSSRG	AGRWKNI	LLGILGGVS	FVWFWDTNE	60								
Db	196	KARGERKEKVHLQ	EALAPKQ	QOQRAQTSSRG	AGRWKNI	LLGILGGVS	FVWFWDTNE	255								
QY	61	EIIMKRRETLANM	CDERARVLQ	QNFVSLNHV	HALSILVSTF	HHGKIPSAID	QRTFEY	120								
Db	256	EIIMKRRETLANM	CDERARVLQ	QNFVSLNHV	HALSILVSTF	HHGKIPSAID	QRTFEY	315								
QY	121	ERTNFERPLTSG	VAYALKVPHS	EREKFEKHG	WAIKKMETED	QTVVQDCVP	ENFDPAPIQ	180								
Db	316	ERTNFERPLTSG	VAYALKVPHS	EREKFEKHG	WAIKKMETED	QTVVQDCVP	ENFDPAPIQ	375								
QY	181	DEYAPVIFAQ	ETVSHIVSD	MMSGEED	RENILRARAS	GKGLTSPFK	LLKSNHLGV	1TF 240								
Db	376	DEYAPVIFAQ	ETVSHIVSD	MMSGEED	RENILRARAS	GKGLTSPFK	LLKSNHLGV	1TF 435								
QY	241	AVYDTSLP	PDPA	TEEQRVEATIG	LGASYDMP	SLVEKLLH	QLASKQ	1TIAVDVYDTNTSGL 300								
Db	436	AVYDTSLP	PDPA	TEEQRVEATIG	LGASYDMP	SLVEKLLH	QLASKQ	1TIAVDVYDTNTSGL 495								
QY	301	IKMYGSEIG	DISQHISS	LDGDP	PSRNHEM	CHRFKHK	LPIPWTAIT	PSILVLVITFLVG 360								
Db	496	IKMYGSEIG	DISQHISS	LDGDP	PSRNHEM	CHRFKHK	LPIPWTAIT	PSILVLVITFLVG 555								
QY	361	ILYEAINRIAT	VEEDCQK	MRELKARAE	AAIAKSQ	FLATVS	HEIRTPMNG	VLGMLKMLMD 420								
Db	556	ILYEAINRIAT	VEEDCQK	MRELKARAE	AAIAKSQ	FLATVS	HEIRTPMNG	VLGMLKMLMD 615								
QY	421	TDLDAKQMD	YAQTAH	SGKDLTSLINE	VDQAKIES	GRLELENV	VPFDMR	FILDNVSSLLS 480								
Db	616	TDLDAKQMD	YAQTAH	SGKDLTSLINE	VDQAKIES	GRLELENV	VPFDMR	FILDNVSSLLS 675								
QY	481	GKANEGIE	LAVYSSQ	VPDVVVG	DP	SRFRQIIT	NLVGNS	IKFTQERGHIFISVHLADEV 540								
Db	676	GKANEGIE	LAVYSSQ	VPDVVVG	DP	SRFRQIIT	NLVGNS	IKFTQERGHIFISVHLADEV 735								
QY	541	KEPLTIED	AVLKOR	LALG	CS	SETVSG	FPAVNA	WGSWK	NKFTCYSTESQ	NSDQIKLLVT 600						
Db	736	KEPLTIED	AVLKOR	LALG	CS	SETVSG	FPAVNA	WGSWK	NKFTCYSTESQ	NSDQIKLLVT 795						
QY	601	VEDTG	VGIPVDAQ	GRIFT	PFMQ	AD	S	TSRTYGGT	GIGLSISK	RLVELMQGEMGFVSEPGI 660						
Db	796	VEDTG	VGIPVDAQ	GRIFT	PFMQ	AD	S	TSRTYGGT	GIGLSISK	RLVELMQGEMGFVSEPGI 855						
QY	661	GSTF	SFTGVFG	KAETNTSIT	KLERFD	LAIQ	EFTGL	RALVID	NRNIRAE	VTRYELRRLGIS 720						
Db	856	GSTF	SFTGVFG	KAETNTSIT	KLERFD	LAIQ	EFTGL	RALVID	NRNIRAE	VTRYELRRLGIS 915						
QY	721	ADIVSS	LRMACTCC	ISKLEN	LAMILID	KDAWN	KEEFS	VLDEL	FTFSKVT	TRVPKIFLLA 780						
Db	916	ADIVSS	LRMACTCC	ISKLEN	LAMILID	KDAWN	KEEFS	VLDEL	FTFSKVT	TRVPKIFLLA 975						
QY	781	TSATL	TERSEM	KSTGLIDE	VVIKPL	RM	SVLIC	CLQ	ETLVN	GKKRQPNRQ	RNLGHLREK 840					
Db	976	TSATL	TERSEM	KSTGLIDE	VVIKPL	RM	SVLIC	CLQ	ETLVN	GKKRQPNRQ	RNLGHLREK 1035					
QY	841	QILV	DDNLV	NR	VAEG	ALKKYG	AI	VTC	VESG	KAALAM	LKP	PHNFAC	FMDLQ	MP	EMDGF 900	
Db	1036	QILV	DDNLV	NR	VAEG	ALKKYG	AI	VTC	VESG	KAALAM	LKP	PHNFAC	FMDLQ	MP	EMDGF 1095	
QY	901	EATRR	VRELER	EIN	KKIAS	GEV	SAEM	FC	FPSS	WHVP	I	L	AMTAD	V	I	QATHEE
Db	1096	EATRR	VRELER	EIN	KKIAS	GEV	SAEM	FC	FPSS	WHVP	I	L	AMTAD	V	I	QATHEE
QY	961	VSKP	FE	EE	EV	LV	LT	AV	AR	FF	EP	CP				

1156 VSKPFEVLYTAVARFFPC 1176

RESULT 2

Q9FKH3

PRELIMINARY;

PRT; 1173 AA.

Q9FKH3;

01-MAR-2001 (Tremblrel. 16, Created)

Q9FKH3;

01-MAR-2001 (Tremblrel. 16, Last sequence update)

Q9FKH3;

01-MAR-2003 (Tremblrel. 23, Last annotation update)

Histidine kinase-like protein.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosid II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

[1]

SEQUENCE FROM N.A.

STRAIN=Columbia;

MEDLINE=98344145; PubMed=9679202;

Kenako T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N., Tabata S.

"Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned pi and TAC clones."

DNA Res. 5:131-145(1998).

EMBL; AB011485; BAB09274.1; -

HSSP; P06143; 1AB6.

InterPro; IPR003594; ATPbind_ATPase.

InterPro; IPR004358; Bact_sens_pr_C.

InterPro; IPR006189; CHASE.

InterPro; IPR003661; His_kinase.

InterPro; IPR005467; His_kinase.

InterPro; IPR001789; Response_reg.

Pfam; PF03924; CHASE; 1.

Pfam; PF02518; HATPase_c; 1.

Pfam; PF00512; Hiska; 1.

Pfam; PF00072; response_reg; 1.

PRINTS; PR00344; BCTRLSENSOR.

ProDom; PD000039; Response_reg; 1.

SMART; SM00387; HATPase_c; 1.

SMART; SM00388; Hiska; 1.

SMART; SM00448; REC; 1.

PROSITE; PS50839; CHASE; 1.

PROSITE; PS50109; HIS_KIN; 1.

PROSITE; PS50110; RESPONSE_REGULATORY; 1.

Kinase; Phosphorylation; Sensory transduction.

SEQUENCE 1173 AA; 131483 MW; 5F6CB4F0848FD1B2 CRC64;

Query Match 99.5%; Score 4991.5; DB 10; Length 1173;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 978; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 KARGERKEKVHLQ EALAPKQ QOQRAQTSSRG AGRWKNI LLGILGGVS FVWFWDTNE 60

Db 196 KARGERKEKVHLQ EALAPKQ QOQRAQTSSRG AGRWKNI LLGILGGVS FVWFWDTNE 255

QY 61 EIIMKRRETLANM CDERARVLQ QNFVSLNHV HALSILVSTF HHGKIPSAIDQRTFEYT 120

Db 256 EIIMKRRETLANM CDERARVLQ QNFVSLNHV HALSILVSTF HHGKIPSAIDQRTFEYT 315

QY 121 ERTNFERPLTSG VAYALKVPHS EREKFEKHG WAIKKMETEDQTVVQDCVPENFDPAPIQ 180

Db 316 ERTNFERPLTSG VAYALKVPHS EREKFEKHG WAIKKMETEDQTVVQDCVPENFDPAPIQ 375

QY 181 DEYAPVIFAQETVSHIVS VDMMSGEEDRENILRARAS GKGLTSPFKLLKSNHLGVLTFF 240

Db 376 DEYAPVIFAQETVSHIVS VDMMSGEEDRENILRARAS GKGLTSPFKLLKSNHLGVLTFF 435

QY 241 AVYDTSLPDPATEEQRVEATIGYLGASYDMP SLVEKLLHQLASKQTIADVYDTNTSGL 300

Db 436 AVYDTSLPDPATEEQRVEATIGYLGASYDMP SLVEKLLHQLASKQTIADVYDTNTSGL 495

QY 301 IKMYGSEIGDISEQHISSLDGDPSPRNHEMHCRCFKHKLPIPWTAITPSILVLVITFLVGY 360
Db 496 IKMYGSEIGDISEQHISSLDGDPSPRNHEMHCRCFKHKLPIPWTAITPSILVLVITFLVGY 555
QY 361 ILYEAINRIATVEEDCQKRELKARAEAAIAKQFLATVSHEIRTPMNGVLGMLKMLMD 420
Db 556 ILYEAINRIATVEEDCQKRELKARAEAAIAKQFLATVSHEIRTPMNGVLGMLKMLMD 615
QY 421 TDLDAKQMDYQAQTAHSGKDLTSLINEVLDAKIESGRLELENVPPDMRFILDNVSSLLS 480
Db 616 TDLDAKQMDYQAQTAHSGKDLTSLINEVLDAKIESGRLELENVPPDMRFILDNVSSLLS 675
QY 481 GKANEKGIELAVVSSQVPDVVVGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 676 GKANEKGIELAVVSSQVPDVVVGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 732
QY 541 KEPLTIEDAVLKQRLALGCSSEGETVSGFPAVNAWGSWKNFKTCYSTESQNSDQIKLLVT 600
Db 733 KEPLTIEDAVLKQRLALGCSSEGETVSGFPAVNAWGSWKNFKTCYSTESQNSDQIKLLVT 792
QY 601 VEDTGVGIPVDAQGRIFTFPMQADSSTSRITYGGTIGLISIKRLVELMQEMGFVSEPGI 660
Db 793 VEDTGVGIPVDAQGRIFTFPMQADSSTSRITYGGTIGLISIKRLVELMQEMGFVSEPGI 852
QY 661 GSTFSFTGVFGKABTNTSITKLERFDLAIQETGLRALVIDNRNIRAEVTRYELRRLGIS 720
Db 853 GSTFSFTGVFGKABTNTSITKLERFDLAIQETGLRALVIDNRNIRAEVTRYELRRLGIS 912
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRPVKIFLLA 780
Db 913 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRPVKIFLLA 972
QY 781 TSATLTERSEMKSTGLIDEVWIKPLRMSVLICLQETLVNGKKRQPNRQRLNGLHLLREK 840
Db 973 TSATLTERSEMKSTGLIDEVWIKPLRMSVLICLQETLVNGKKRQPNRQRLNGLHLLREK 1032
QY 841 QILVDDNLVNRRAEAGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 900
Db 1033 QILVDDNLVNRRAEAGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 1092
QY 901 EATRRVRELEREINKKIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEECMCKGMDGY 960
Db 1093 EATRRVRELEREINKKIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEECMCKGMDGY 1152
QY 961 VSKPFEVEEVLYTAVARFFEP 981
Db 1153 VSKPFEVEEVLYTAVARFFEP 1173

RESULT 3
Q8GUG0 PRELIMINARY; PRT; 652 AA.
AC Q8GUG0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Histidine kinase-like protein.
GN AT5G35750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,
RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,
RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,
RA Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
RA Davis R.W.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BT002530; AAO00890.1; --
KW Kinase.
SQ SEQUENCE 652 AA; 72656 MW; 705751BAA15C4E05 CRC64;
Query Match 66.1%; Score 3316; DB 10; Length 652;
Best Local Similarity 100.0%; Pred. No. 4.9e-210;
Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 330 MHCRFKHKLPIPWTAITPSILVLVITFLVGYILYEAINRIATVEEDCQKRELKARAEAA 389
Db 1 MHCRFKHKLPIPWTAITPSILVLVITFLVGYILYEAINRIATVEEDCQKRELKARAEAA 60
QY 390 DIAKSQFLATVSHEIRTPMNGVLGMLKMLMDTDLDAKQMDYQAQTAHSGKDLTSLINEVL 449
Db 61 DIAKSQFLATVSHEIRTPMNGVLGMLKMLMDTDLDAKQMDYQAQTAHSGKDLTSLINEVL 120
QY 450 DQAKIESGRLELENVPPDMRFILDNVSSLLSGKANEKGIELAVVSSQVPDVVVGDPSPR 509
Db 121 DQAKIESGRLELENVPPDMRFILDNVSSLLSGKANEKGIELAVVSSQVPDVVVGDPSPR 180
QY 510 RQIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSSEGETVSGF 569
Db 181 RQIITNLVGNISIKFTQERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSSEGETVSGF 240
QY 570 PAVNAWGSWKNFKTCYSTESQNSDQIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSTSR 629
Db 241 PAVNAWGSWKNFKTCYSTESQNSDQIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSTSR 300
QY 630 TYGGTIGLISIKRLVELMQEMGFVSEPGIGSTFSFTGVFGKABTNTSITKLERFDLAI 689
Db 301 TYGGTIGLISIKRLVELMQEMGFVSEPGIGSTFSFTGVFGKABTNTSITKLERFDLAI 360
QY 690 QEFTGLRALVIDNRNIRAEVTRYELRRLGISADIVSSLRMACTCCISKLENLAMILIDKD 749
Db 361 QEFTGLRALVIDNRNIRAEVTRYELRRLGISADIVSSLRMACTCCISKLENLAMILIDKD 420
QY 750 AWNKEEFSVLDELFTRSKVTFTRPVKIFLLATSATLTERSEMKSTGLIDEVWIKPLRMSV 809
Db 421 AWNKEEFSVLDELFTRSKVTFTRPVKIFLLATSATLTERSEMKSTGLIDEVWIKPLRMSV 480
QY 810 LICCLQETLVNGKKRQPNRQRLNGLHLLREKQILVDDNLVNRRAEAGALKKYGAIVTCV 869
Db 481 LICCLQETLVNGKKRQPNRQRLNGLHLLREKQILVDDNLVNRRAEAGALKKYGAIVTCV 540
QY 870 ESGKAALAMLKPPHNFDA CFMDLQMPMDGF EATRRVRELEREINKKIASGEVSAEMFCK 929
Db 541 ESGKAALAMLKPPHNFDA CFMDLQMPMDGF EATRRVRELEREINKKIASGEVSAEMFCK 600
QY 930 FSSWHVPILAMTADVIQATHEECMCKGMDGYVSKPFEVEEVLYTAVARFFEP 981
Db 601 FSSWHVPILAMTADVIQATHEECMCKGMDGYVSKPFEVEEVLYTAVARFFEP 652

RESULT 4
Q8L8I6 PRELIMINARY; PRT; 1041 AA.
AC Q8L8I6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cytokinin receptor.
GN CKR1.
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
OC Catharanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22166729; PubMed=12177139;
RA Papon N., Clastre M., Andreu F., Gantet P., Rideau M., Creche J.;
RT "Expression analysis in plant and cell suspensions of CrCKR1, a cDNA

Db 92 WRK-LVVVVVFWVLVSIWTFWYFSSQAMEKRRKETLASMCDERARMLQDQFNVSMNHVQA 150
QY 95 LSLIVSTFHHGKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSERKEKFEKHGWA 154
Db 151 MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEREERQQGW 210
QY 155 IKKMETEDQTVV--QDCVPENFDPAPIQDEYAPVIFAQETVSHIVSDMMSGEEDRENIL 212
Db 211 IRKMSLEQNPHKDDYDLEALERSPVQDEYAPVIFAQDTVSHVSLDMLSGKEDRENVL 270
QY 213 RARASGKGLTSPFPKLLKSNHLGVLTFAVYDTSPPDATEEQRVEATIGYLASYSMP 272
Db 271 RARSSGKGLTAPFPPLIKTNRLGVILTFAYVKRDLPSNATPKERIEATNGYLGGVFDIES 330
QY 273 LVEKLLHQLASKQTIADVVDYDTTNTSGLIKMYGSEIGDISEQHISSLDGDPSPRNHEMH- 331
Db 331 LVENLLQLASKQTIILNVYDITNHSQIPSMYGTNVSADGLERSVPLIFGDLRKHEMRC 390
QY 332 -----CRFKHKLPIPWTAITPSILVLVITFLVGY 360
Db 391 RYLQLAHTYVCNFFLFARIOVLTFCCELLPLCRFKQKPPWPVLSMVTSGILVIALLVAH 450
QY 361 ILYEAINRIATVEEDCQKRELKARAEADIAKSQFLATVSHEIRTPMNGVLGMLKMLMD 420
Db 451 IIHATVSRIRHKVEEDCDKMQLKKAEEADVAKSQFLATVSHEIRTPMNGVLGMLHMLMD 510
QY 421 TOLDAKQMDYAQTAAHSGKDLTSLINEVLDQAKIESGRLELENVPPDFRILDNVSSLLS 480
Db 511 TELDVTQDQYVRTAASGKALVSLINEVLDQAKIESGKLEEEVRFDLGILDVLSLFS 570
QY 481 GKANEGIELAVYSSQVDPVVVGDPSPFRFOITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 571 SKSQQGVVELAVISDRVPMGLIGDPGRFOITNLMGNSIKFT-EKGHIFVTVHLVDEL 629
QY 541 KEPLTIEDAVLKQRLALGCSEGETVSGFPAVNAWSWKNFKTCYSIESQNS-----DQI 595
Db 630 PESIDGETA-----SSPESTLSGLPVADRQRSWENFK-AFSSNGHRSFEPSPDDI 678
QY 596 KLLVTVEDTGVIPVDAQGRIFTPFMQADSTSTRTYGGTGIGLSISKRLVELMQGEMGV 655
Db 679 NLIVSVEDTGVIPVEAQSRIFTPFMQVGPISRTHGGTGIGLSISKCLVGLMKGEIGFS 738
QY 656 SEPGIGSTFSGTVPG-----KAETNTSITKLERFDLAIQEFTGLRALVIDNRNIRA 707
Db 739 STPKVGSTFTFTAVFSGMQPAERKNDNNQPI-----FSEFRGMKAVVVDHRPARA 789
QY 708 EVTRYELRLGISADIVSSLSRMACTCCISKLENLAMILIDKDAWNKEEFSVLDLFTRSK 767
Db 790 KVSWYHFQRLGIRVEVVRVEQALHYLKIGTTVNMILIEQEIWNREADDFIKKL--QK 846
QY 768 VTFTRPVKIFLLATSATLTERSEMSTGLIDE--VVIKPLRMSVLICCUQETLVNGKKRQ 825
Db 847 DPLFLSPKLILLANSVE-SSISEALCTG-IDPFIVIVKPLRASMLAATLQRLGIGIREP 904
QY 826 PNRQ--RRNLGHLIREKQILVVDNVLNRRVAEGALKKYGAIVTCVESGKAALAMLKPP 882
Db 905 PQHKGPPALILRNLLGRKILIVDDNNVNLRAAGALKKYGADVVCAESGIIKALSLLKPP 964
QY 883 HNFDAFCMDLQMPMDGFEATRVRRELEREINKKIASGEVSAEMFCKFSWHVPILAMTA 942
Db 965 HEFDACFMDIQMPMDGFEATRRIIRDMEEMNKRIKNGEALIVENGKTSWHLPVLAMTA 1024
QY 943 DVIQATHEECMKCGMDGY 960
Db 1025 DVIQATHEECLKCGMDGY 1042

RESULT 7

Q8RYG4
ID Q8RYG4 PRELIMINARY; PRT; 1023 AA.
AC Q8RYG4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative histidine kinase.
GN P0592G05.13.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC
RT clone:P0592G05.";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004672; BAB90827.1; -.
DR Gramene; Q8RYG4; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1023 AA; 113219 MW; 469AC35146CDF62B CRC64;

Query Match 51.3%; Score 2575; DB 10; Length 1023;
Best Local Similarity 54.7%; Pred. No. 7.3e-161;
Matches 545; Conservative 136; Mismatches 251; Indels 64; Gaps 18;

QY 18 PKKQQQRAQTSSRGA-----GRWRKN-----ILLGILGVSFVVMFWDNTEEIIMKR 66
Db 52 PEKVSARARV-VRGSLVAHFRGWRVVRRETWWVLLWILAGSLGSFYLFMFMAQSLDKR 110
QY 67 RETLANMCDERARVLQDQFNVSINHVHALSILVSTFHHGKIPSAIDQRTFEEYTERTNFE 126
Db 111 RDSLASMCDERARMLQDQFNVSMNHLQALAILVSTFHHSKTSPSAIDQMTFARYAERTAFE 170
QY 127 RPLTSGVAYALKVPHSEREREKFEKHGWAIIKKMETEDQTVVQDCVPENFDPAPIQ----D 181
Db 171 RPLTSGVAYAVRVTHGEREQFERQQGWAIIKMYSSSNKKQSSPGPGDAAVAEIREPAE 230
QY 182 EYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFPKLLKSNHLGVLTFA 241
Db 231 EYAPVIFAQDAYKHVISDFMLSGNEDRDNILRARKSGKGLTAPFKLL-NNRLGVILTYT 289
QY 242 VYDTSLPDATEEQRVEATIGYLASYSMPSLVEKLLHQLASKQTIADVVDYDTTNTSGLI 301
Db 290 VYKYELPAYARPHERIQAAIGYLGIGFDIQALVEKLLKQLASQESIMVNVDYDTTNESP-I 348
QY 302 KMYGSEIGDISEQHISSLDGDPSPRNHEMHCRFKHKLPIPWTAITPSILVLVITFLVGYI 361
Db 349 SMYGGDTGS-GMCHVSVLNFQDPSRKHEMHCRFEKKPPWPWLAITSSFGTLVIALLTGHI 407
QY 362 LYEAINRIATVEEDCQKRELKARAEADIAKSQFLATVSHEIRTPMNGVLGMLKMLMDT 421
Db 408 FQATVHRIAKVEDDDFKMSELKKAEDADVAKSQFLATVSHEIRTPMNGVLGMLQMLMDT 467
QY 422 DLDKQMDYAQTAAHSGKDLTSLINEVLDQAKIESGRLELENVPPDFMRFILDNVSSLLSG 481
Db 468 DLDTTQDQYVRTAASGKALVSLINEVLDQAKIESGKLEETVPFDLRTVCDDILSLFCG 527
QY 482 KANEGIELAVYSSQVDPVVVGDPSPFRFOITNLVGNISIKFTQERGHIFISVHLADEVK 541

SQ	SEQUENCE	1080 AA; 120730 MW; 5950DB968B529401 CRC64;
	Query Match	50.6%; Score 2539.5; DB 10; Length 1080;
	Best Local Similarity	53.2%; Pred. No. 1.8e-158;
	Matches	537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;
QY	4	GERKEVHLQE--ALAPKKQQQRAQTSSRGAGRWRKNILLGILGGVSPVW-WFWDTNE 60
Db	112	GNKKGSTFIQEHRAALLPKAL-----ILWIIIVGFSSGIYQWMDANK 154
QY	61	EIIMKRRETLANMCDERARVLQDQFNVS LNHVHALSILVSTFHHGKIPSAIDQRTFEY 120
Db	155	---IRREEVLVSMCDQARMLQDQFSVNVHVALAILVSTFHHKNPSAIDQETFAEY 211
QY	121	ERTNFERPLTSGVAYALKVPHSEREKEFEKEHGWAIKKMETEDQTVVQDCVPENFDPA 180
Db	212	ARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTM-----DRGEPSPVR 258
QY	181	DEYAPVIFAQETVSHIVSVDMMSGEEDRENILRARASGKGVLTSPFKLLKSNHLGV 240
Db	259	DEYAPVIFSQDSVSYLES LDDMMSGEEDRENILRARETGKAVLTSPRLLETHHLGV 318
QY	241	AVYDTSLPDATEEQRVEATIGYLGASVDMPSLVEKLLHQLASKQTIADVVDYDTNTS 300
Db	319	PVYKSSLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNQAIVVHVYDITNAS 378
QY	301	IKMYGS--EIGDISEQHISSLDGDPDSRNHEMHCRCFKLPIPTWTAITPSILVLV 358
Db	379	LVMYGNQDEADRSLSHESKLDGDPFRKHMKICRYHQKAPIPLNVLTTPFLFAIG 438
QY	359	GYILYEAINRIATVEEDCQKRELKARAAADIASKQFLATVSHEIRTPMNGVLGML 418
Db	439	GYILYGAAHVIKVDEDDFHEMQELKVRABAAADVAKSQFLATVSHEIRTPMNGIL 498
QY	419	MDTDLDKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFILDNV 478
Db	499	LDTELSSTQRDYAQTAVQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSIL 558
QY	479	LSGKANEEKIELAVYVSSQVDPVVVGDPSPFRQIITNLVGNISIKFTQERGHIFIS 538
Db	559	FSEESRNKSIELAVFVSDKVPEIVKGDGSRFRQIINLVGNSVKFT-EKGHIFVKV 617
QY	539	EVK---EPL-TIEDAVLKQRLALGCSEGETVSGFPVNAWGSWKNFKTCYSTESQNS 593
Db	618	QSKDESEPKNALGGVSEEMIVSVKQSSYNTLSGYEADGRNSWDFKHLVSEEQSLSE 677
QY	594	---QIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSTSRTYGGTGIGLSISKRLV 649
Db	678	DISSNVRLMVSIEDTGIGIPLVAQGRVFMFPQADSSTSRNYGGTGIGLSISKCLV 737
QY	650	GEMGFVSEPGIGSTFSTGVFGKAEFNTSITKLER--FDLAIQBEFTGLRALVIDNR 707
Db	738	GQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKKNVEHLPSTPKGMKAIVVDAKP 797
QY	708	EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKDAW----- 753
Db	798	AVTRYHMKRLGINVDVWTSKTAVVAAAFAERNGPSLPTKPQLDMILVEKDSWISTE 857
QY	754	EEFSVLDELFTRSKVTFTRPVKIFILLATSATLTERSEMKS TGLIDEVVIKPLRMSV 813
Db	858	SEIRLLNSR-TNGNV-HHKSPKALFATNITNSEFDRAKSAGFADTVMKPLRSMIGAC 915
QY	814	LQETLVNGKKQPNRQRN--LGHLLREKQILVDDNLVNRRAEGALKKYGAIVTCVE 870
Db	916	LQQVLELRKTRFQQHPEGSSPATLTKSLLTGKKILVDDNIVNRRVAAGALKKFGAE 975
QY	871	SGKAALAMLKPPHNFDA CFMDLQMPENDGFEATRVRRELEREINKKIASGEVSAEM 930
Db	976	SGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKETKNTN----- 1023
QY	931	SSWHVPILAMTADVIOATHEECMKCGMDGVYVKPFEFEEVLYTAVARFFEP 980
Db	1024	LEWHLPILAMTADVIHATYEECLKSGMDGVYVKPFEFEEENLYKSAKSFKP 1073

RESULT 12

Q8S6P5

ID	Q8S6P5	PRELIMINARY;	PRT;	925 AA.
AC	Q8S6P5;			
DT	01-JUN-2002	(TrEMBLrel. 21, Created)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)		
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)		
DE	Putative histidine kinase.			
GN	OSJNBA0073L01.1.			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
OX	NCBI_TaxID=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Nipponbare;			
RA	Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,			
RA	Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,			
RA	Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,			
RA	Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,			
RA	Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;			
RT	"Oryza sativa chromosome 10 BAC OSJNBA0073L01 genomic sequence.";			
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AC092548; AAM18726.1; -.			
DR	Gramene; Q8S6P5; -.			
DR	InterPro; IPR003594; ATPbind_ATPase.			
DR	InterPro; IPR006189; CHASE.			
DR	InterPro; IPR003661; His_kinA.			
DR	InterPro; IPR005467; His_kinase.			
DR	InterPro; IPR001789; Response_reg.			
DR	Pfam; PF03924; CHASE; 1.			
DR	Pfam; PF02518; HATPase_c; 1.			
DR	Pfam; PF00512; Hiska; 1.			
DR	Pfam; PF00072; response_reg; 1.			
DR	ProDom; PD000039; Response_reg; 1.			
DR	SMART; SM00387; HATPase_c; 1.			
DR	SMART; SM00388; Hiska; 1.			
DR	SMART; SM00448; REC; 1.			
DR	PROSITE; PS50839; CHASE; 1.			
DR	PROSITE; PS50109; HIS_KIN; 1.			
DR	PROSITE; PS50110; RESPONSE_REGULATORY; 2.			
KW	Kinase; Phosphorylation; Sensory transduction.			
SQ	SEQUENCE 925 AA; 102928 MW; 6046D9AC28824219 CRC64;			

Query Match

Best Local Similarity 59.5%; Score 2520; DB 10; Length 925;

Matches 520; Conservative 116; Mismatches 216; Indels 22; Gaps 9;

QY	61	EIIMKRRETLANMCDERARVLQDQFNVS LNHVHALSILVSTFHHGKIPSAIDQRTFE 120
Db	4	DVVARRIENLENMCDERARMLQDQFNVS MNHVHALAILVSTFHHGKNPSAIDQKTF 63
QY	121	ERTNFERPLTSGVAYALKVPHSEREKEFEKEHGWAIKKMETEDQTVVQDCVPENFD 180
Db	64	ARTTFRPLMSGVAYALKVLHLSERELFEQKLGWKIKKMETEDQSLVHDYNPEKLPSP 123
QY	181	DEYAPVIFAQETVSHIVSVDMMSGEEDRENILRARASGKGVLTSPFKLLKSNHLGV 240
Db	124	DEYAPVIFSQETVKHIIISVDMMSGEKDRDNILRSRATGKALTAPFPLKSNHLGV 183
QY	241	AVYDTSLPDATEEQRVEATIGYLGASVDMPSLVEKLLHQLASKQTIADVVDYDTNT 300
Db	184	TVYKYDLPDPATPEERIEATLGYLGASFDVPSPSLVERLLEQLASKQIVVRLYDIT 243
QY	301	IKMYGSEIGDISEQHISSLDGDPDSRNHEMHCRCFKLPIPTWTAITPSILVLVITF 360
Db	244	TKMYSDSVIASDDLHISNIDFGDPTRKHVHMCRCFKHAPSLPWSAIMISSAVAIL 303
QY	361	ILYEAINRIATVEEDCQKRELKARAAADIASKQFLATVSHEIRTPMNGVLGMLKML 420

Db 304 IYATLNSLEAEADNYTTMRDLKGRAEAADVAKSQFLATVVSHEIRTPMNGVLGMLQMLMD 363

QY 421 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFILDNVSSLLS 480

Db 364 TELDTTQDRFVVTAQESGSLINLINEVLDLAKIESKIELEAVRFDVRDILDNVVSLSFS 423

QY 481 GKANEKGIELAVYVSSQVPDVVGDPSRFRQIITNLVGNISIKFTQERGHIFISVHladev 540

Db 424 EKSWAKGIELAVLSQVDPVLIGDPWRFRQIITNLVGNsmkft-EQGHIFIRVHLIEEV 482

QY 541 KEPLTIEDAVLKQRLALCCSESG----ETVSGFPVAVNAWGSWKNFKTCYSTESQSDQIK 596

Db 483 KRQWEALDDTSPENIEVTANSKNTMPYNTLSGLEVANNRKTLESFR-MFKDSSDAIDSVN 541

QY 597 LLVTVEDTGVGIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQEMGFVS 656

Db 542 LLVTVEDTGIGITKDAQTRIFTPFMQADGSTSRTYGGTGIGLSITKRLVELMGGEIGFVS 601

QY 657 EPGIGSTFSFTGVFGKAETNTSITKLERFDLAIQBFDTGLRALVIDNRNIRAETRYELRR 716

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QY 717 LGISADIVSSLRMAC-----TCCISKLENLAMILIDKAWNKEE----FSVLDELFTRSK 767

Db 662 LGIQCDLAATSESALSALLESCNSSVKSSLNMLVVDKEAWGEDSGLAFFRCLIDLRLKGT 721

QY 768 V-TFTRVPKIFILLATSATLTERSEMSTGLIDEVVIKPLRMSVLICCLQETLVNGKKRQP 826

Db 722 LKSWQTMPKFFLLAGSITPADSDCLRLAGYSNS-TRKPLRLSTVAACLSKAL--GVGLTG 778

QY 827 NRQRRN---LGHLLREKQILVDDNLVNRRAEGALKKYGAIVTCVESGKAALAMLKPPH 883

Db 779 RRSRDNSLVRSLTGKNILVDDNAVNRIVAAGALKKYGAIVTCVDSGKEAISRLQPPH 838

QY 884 NFDACFMDLQMPMDGFEATRVRRELEREINKKI 917

Db 839 KFDACFMDVQMPMDGFEATRLVRSVESKINDTI 872

RESULT 13
Q9FRY7

ID Q9FRY7 PRELIMINARY; PRT; 974 AA.

AC Q9FRY7;

DT 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DE Histidine kinase 1.

GN ZMHK1.

OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

OX NCBI_TaxID=4577;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Golden Cross Bantam T51;

RA Sakakibara H., Sugiyama T.;

RT "Cloning and characterization of maize response regulators.";

RL Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases.

DR EMBL; AB042270; BAB20583.1; -.

DR HSSP; P06143; 1AB6.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR004358; Bact_sens_pr_C.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR PRINTS; PR00344; BCTRLSENSOR.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW Kinase; Phosphorylation; Sensory transduction.

SQ SEQUENCE 974 AA; 108074 MW; 3EF67B0202D839F0 CRC64;

Query Match 47.1%; Score 2363; DB 10; Length 974;

Best Local Similarity 50.8%; Pred. No. 6.5e-147;

Matches 503; Conservative 152; Mismatches 251; Indels 84; Gaps 18;

QY 34 RWRKNILLG-ILGGVSFSVWFWDTNEELIMKRRETLANMCDERARVLQDFNVSLNHV 92

Db 12 RWRGLAAAGWVLTAVCSAVMHWTLRRDSMDRAEERLVSMCEERARNLQEQFGVTNVHV 71

QY 93 HALSILVSTFHHGKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSEREKFEKEHG 152

Db 72 HAAIILISTFNFEPKSPPAIDQDTFAKYTARTSFERPLLNQVAFARQVFRHEREMPESQQG 131

QY 153 WAKKMETEDQTVVQDCVPENFDPAPIQDEYAPVIFAQETVSHIVSDVMMSGEEDRENIL 212

Db 132 WVMNTMQRE-----PAPQVEYAPVIFSQDTSYLARIDMMSGEEDRENIF 177

QY 213 RARASGKGLTSPPKLLKSNHLGVLTFAVYDTSLPDATEEQRVEATIGYLASVDMP 272

Db 178 RARTTGKAVLTNPFRLLSNHLGVLTFAVYRDPDLPADASVEQORVEATIGYLGAFDVES 237

QY 273 LVEKLLHQLASKQTIADVDTTNTSGLIKMYGSEIGDISEQ-----HISLDFGDP 328

Db 238 LVENLLSKLAGNQDIVNVYDVTNASDAMVLYGP--SSLDEQVPFLHVSMLDFGDPFRKH 295

QY 329 EMHCRFKHLPIPTAITPSILVLVITFLVGILYEAINRIATVEEDCQKRELKARAEA 388

Db 296 EMRCRYRQKLEMPWSAITNPLGTFVIWMLLGYISIAAAYSRYDKVTEDCRKMEELKTQAEA 355

QY 389 ADIAKSQFLATVSHEIRTPMNGVLGMLKMLMDTDLDAKQMDYAQTAHSGKDLTSLINEV 448

Db 356 ADVAKSQFLATASHEIRTPMNGVLGMLDMLLGLTDLTMTQKDYAQTAQMCGRALITLINDV 415

QY 449 LDQAKIESGRLELENVPFDMRFILDNVSSLLSGKANEGIELAVYVSSQVPDVVVGDP 508

Db 416 LDRAKIEAGKLELEAVPFDLRSLMDDVVSFLFSSKSREKCIELAVFVCDNVPKVIGDPWR 475

QY 509 FRQIITNLVGNISIKFTQERGHIFISVHladevKEPLTIEDAVLKQRLALCCSESGE--- 564

Db 476 FRQILTNLVGNAVKET-ERGHVFRVCLA-----ENSMEANQVLHGAMNGKGRV 525

QY 565 -----TVSGFPVAVNAWGSWKNFKTCYS-----TESQN-----SDQIKLLVTVE 602

Db 526 ESTANGAFNTLSGFEAADRRNSWQYFKLLSLDSKESLLDDLESENNSQSDSDRVTLAISIE 585

QY 603 DTGVGIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQEMGFVSEPGIGS 662

Db 586 DTGVGIPLQADRVFTPFMQADSSSTRNYGGTGIGLSISKCLAEMLMGQGISFTSHPSVGS 645

QY 663 TFSFTGVFGKAETNTSITKLERFDLAI-QEFTGLRALVIDNRNIRAETRYELRRLGISA 721

Db 646 TFTFSATLKXSHKDISGDSSRSLTEALPTAFKGMKAILVDGRPVRSVATRYHLKRLGILL 705

QY 722 DIVSSLRMACTC-----CISKLENLAMILIDKAWNKE-EFSVLDELFTRSKVTFTRVP 774

Db 706 QVVNNMNAVVKAPFGQNGAAGSREKASILFIESDFWRPETDVQLLNHLREKQNGQLSDGH 765

QY 775 KIFLLATSATLTERSEMSTGLIDEVVIKPLRMSVLICCLQETL-VNGKKRQPNRQRN- 832

Db 766 KVVLLVTS-----EADKDKYGSIFDIVMCKPIRASTIASIIQQLLKVEIAERKDNQNRPSF 821

QY 833 LGHLLREKQILVDDNLVNRRAEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDL 892

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Db 898 ELAVSEAHFKALFDGATIGIV--NVDIKGLILDNCYQFCEDMGLS---RDELRSTPIFDV 952

QY 304 YGSEIGDISEQHISSLDGDPSPRNHEMHCRFKHKLPIP-----WTAITPSILVLVITFLV 358

Db 953 LSAQDKDVAKAQFKELVEGKID-----HYRGERSFVRPSGEPLWMTVNVSTLL----- 1000

QY 359 GYILYEAINRIATVEEDCQKMRELKA-----RAEAADIAKSQFLATVVSHEIRTPM 408

Db 1001 -----DSQNQFESAVVSMVDMTELKLLSDELLVAKDEADAASKAKGDFLANNMSHEIRTPM 1055

QY 409 NGVLGMLKMLMDTDLDAKQMDYAAQTAHSGSKDLTSLINEVLDQAKIESGRLELENVPPDM 468

Db 1056 NAIIGMSQLCLQTQLDKQKNVLEKIERASQSLLSIINDILDFSKIEAGKLDIENVSFQL 1115

QY 469 RFIIDNVSSLLSGKANEKGIELAVVSSQVPDVVVGDPSPRFRQIITNLVGNISIKFTQERG 528

Db 1116 DTWLEDLSDMFSERAAQKQIELLFAPA PNPVRHLLGDPLRLGQVLINLMNNAIKFT-ERG 1174

QY 529 HIFISVHLADEVKEPLTIEDAVLKQRLALGCSESETVSGFPAPVNAWGSWKNFKTCYSTE 588

Db 1175 EVLLSLSLVE----- 1184

QY 589 SQNSDQIKLLTVTEDTGVGIPVDAQGRIFTPFMQADSSTSRTYGGTGIGLSISKRLVELM 648

Db 1185 -QONDVVLRFSVRDSGIGLTQEQQSKLFKSFTQADTSTRKYGGTGLGLAISQQLVELM 1243

QY 649 QGEMGFVSEPGIGSTFSFTGVFGKAETNTSITKLERFDLAIQEFTGLRALVIDNRNIRAE 708

Db 1244 GGSIGVESQLGHGSTFFFT-----VKLCISSGQKLFVG-QELDGMSILVADDNATARD 1295

QY 709 VTRYELRRLGISADIVSSILRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKV 768

Db 1296 IMRTTLESMGFNVDTVRSGDEAIMRC--SQQEYAVALIDWKMPNLDGIETAKQIKQTK- 1352

QY 769 TFTRVPKIFLLATSATLTERSEMKSSTGLIDEVVIKPLRMSVLI CCLQETLVNGKKRQPNR 828

Db 1353 ---NAPRILMVSAHANQDFTQIEQLGLAG-YISKPTISASRLLDGIMNALGRSGILPVRR 1408

QY 829 QRRNLGH----LLREKQILVVDDNLVNRRAEGALKKYGAIVTCVESGKAALAMLKPPHN 884

Db 1409 HQDNIAPELLPLKGRILLVEDNEMNLEVATEFLEQVGIILSIATNGQIALDKL-AQOS 1467

QY 885 FDACFMDLQMPMDGFETRRVRELEREINKKIASGEVSAEMFCKFSSWHVPILAMTADV 944

Db 1468 FDLVLMDCQMPVMDGYQATKAIRQ-----RPELA-----QLPVIAMTANA 1507

QY 945 IQATHEECMKCGMDGYVSKPPEEEVLYTAVARF 977

Db 1508 MAGDKEMCLRAGMNDHIAKPIEVNLLYQTLLKY 1540

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:18 ; Search time 36.7512 Seconds
(without alignments)
4236.886 Million cell updates/sec

Title: US-09-918-508-2_COPY_196_1176
Perfect score: 5019
Sequence: 1 KARGERKEKVLQELAPKK.....SKPPEEEVLYTAVARFFEP 981

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5019	100.0	1132	21	Arabidopsis thaliana
2	5019	100.0	1176	21	Arabidopsis thaliana
3	5019	100.0	1176	23	A. thaliana cytoki
4	5019	100.0	1176	24	Arabidopsis thaliana
5	5019	100.0	1238	21	Arabidopsis thaliana
6	4991.5	99.5	1173	23	Wooden leg (WOL) g
7	4991.5	99.5	1173	23	Herbicideally activ
8	2685.5	53.5	1036	23	A. thaliana cytoki
9	2685.5	53.5	1036	24	Arabidopsis thaliana

10	2595.5	51.7	1092	23	AAO22567	Wooden leg (WOL) g
11	2595.5	51.7	1092	23	ABB91150	Herbicideally activ
12	2545.5	50.7	1057	23	ABG70783	A. thaliana cytoki
13	2539.5	50.6	1057	23	AAO22558	Wooden leg (WOL) g
14	2539.5	50.6	1057	23	AAO22570	Wooden leg (WOL) g
15	2539.5	50.6	1057	24	AAE33694	Arabidopsis thalia
16	2534.5	50.5	1057	24	AAE33696	Arabidopsis thalia
17	2531.5	50.4	1057	24	AAE33695	Arabidopsis thalia
18	1502.5	29.9	600	23	ABB91688	Herbicideally activ
19	1132.5	22.6	426	21	AAB25156	Eucalyptus grandis
20	1010.5	20.1	412	21	AAB25530	Eucalyptus grandis
21	860	17.1	274	23	AAO22561	Wooden leg (WOL) g
22	844	16.8	289	23	AAO22563	Wooden leg (WOL) g
23	731.5	14.6	1298	19	AAW68522	N. crassa oslp pro
24	731.5	14.6	1298	20	AAW28481	osl+p amino acid s
25	720.5	14.4	1281	20	AAW28484	osl histidine kina
26	720.5	14.4	1298	20	AAW28483	osl histidine kina
27	693	13.8	1081	20	AAW28482	cos-1 histidine ki
28	687	13.7	1081	20	AAW81600	Candida albicans C
29	642.5	12.8	2150	23	AAO22566	Wooden leg (WOL) g
30	594.5	11.8	1018	21	AAB25534	Eucalyptus grandis
31	579.5	11.5	922	22	AAB73274	Histidine protein k
32	579.5	11.5	922	22	AAB73275	Histidine protein k
33	578.5	11.5	922	22	AAB73276	Histidine protein k
34	563.5	11.2	971	20	AAW88480	Candida albicans h
35	563.5	11.2	2471	20	AAW88481	Candida albicans h
36	553.5	11.0	950	23	ABB93422	Herbicideally activ
37	537	10.7	666	24	AAO26994	Pseudomonas aerugi
38	537	10.7	709	24	AAO26993	Pseudomonas aerugi
39	537	10.7	719	24	AAO26992	Pseudomonas aerugi
40	537	10.7	802	24	AAO26991	Pseudomonas aerugi
41	537	10.7	870	24	AAO26990	Pseudomonas aerugi
42	537	10.7	874	24	AAO26989	Pseudomonas aerugi
43	537	10.7	887	24	AAO26988	Pseudomonas aerugi
44	537	10.7	900	24	AAO26987	Pseudomonas aerugi
45	537	10.7	906	24	AAO26986	Pseudomonas aerugi

ALIGNMENTS

RESULT 1

AAG47090

ID AAG47090 standard; Protein; 1132 AA.

XX AAG47090;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 59314.

DE Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 08-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
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PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.

PR	14-OCT-1999;	99US-0159330.	Query Match Best Local Similarity 100.0%; Score 5019; DB 21; Length 1132; Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
PR	14-OCT-1999;	99US-0159331.		
PR	14-OCT-1999;	99US-0159637.		
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PR	18-OCT-1999;	99US-0159584.		
PR	21-OCT-1999;	99US-0160741.		
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PR	22-OCT-1999;	99US-0160989.		
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PR	26-OCT-1999;	99US-0161359.		
PR	26-OCT-1999;	99US-0161360.		
PR	26-OCT-1999;	99US-0161361.		
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PR	28-OCT-1999;	99US-0161992.		
PR	28-OCT-1999;	99US-0161993.		
PR	29-OCT-1999;	99US-0162142.		
QY	1	KARGERKEKVHLOEALAPKKQQQRAQTSSRGAGRWKRNILLGILGGVSFSVWFWDTNE	60	
Db	152	KARGERKEKVHLOEALAPKKQQQRAQTSSRGAGRWKRNILLGILGGVSFSVWFWDTNE	211	
QY	61	EIIMKRRETLANMCDERARVLQDQFNVSLNHVHALSILVSTFHHGKIPSAIDQRTFEY	120	
Db	212	EIIMKRRETLANMCDERARVLQDQFNVSLNHVHALSILVSTFHHGKIPSAIDQRTFEY	271	
QY	121	ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ	180	
Db	272	ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ	331	
QY	181	DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHLGVLT	240	
Db	332	DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHLGVLT	391	
QY	241	AVYDTSLPDATEEQRVEATIGYLGASYDMPSLVEKLLHLQASKQTIADVYDTTNTSGL	300	
Db	392	AVYDTSLPDATEEQRVEATIGYLGASYDMPSLVEKLLHLQASKQTIADVYDTTNTSGL	451	
QY	301	IKMYGSEIGDISEQHISSLDFGDPSRNHEMHC RFKHLPIPWTAITPSILVLVITFLVG	360	
Db	452	IKMYGSEIGDISEQHISSLDFGDPSRNHEMHC RFKHLPIPWTAITPSILVLVITFLVG	511	
QY	361	ILYEAINRIATVEEDCQKMRELKARAEAA DIAKSQFLATVSHEIRTPMNGVLGMLKMLD	420	
Db	512	ILYEAINRIATVEEDCQKMRELKARAEAA DIAKSQFLATVSHEIRTPMNGVLGMLKMLD	571	
QY	421	TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVFPDMRFILDNVSSLLS	480	
Db	572	TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVFPDMRFILDNVSSLLS	631	
QY	481	GKANKEGIELAVYVSSQVPDVVVGDPSPRFRQIITNLVGN SIKFTQERGHIFISVHLADEV	540	
Db	632	GKANKEGIELAVYVSSQVPDVVVGDPSPRFRQIITNLVGN SIKFTQERGHIFISVHLADEV	691	
QY	541	KEPLTIEDAVLKQRLALGCSEGETVSGFPAPNAWGSWKNFKTCYSTESQNSDQIKLLVT	600	
Db	692	KEPLTIEDAVLKQRLALGCSEGETVSGFPAPNAWGSWKNFKTCYSTESQNSDQIKLLVT	751	
QY	601	VEDTGVGIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI	660	
Db	752	VEDTGVGIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI	811	

QY	661	GSTFSFTGVFGKAE TNTSITKLERFDLAIQEFTGLRALVIDNRNIRA EVTRYELRRLGIS	720	
Db	812	GSTFSFTGVFGKAE TNTSITKLERFDLAIQEFTGLRALVIDNRNIRA EVTRYELRRLGIS	871	
QY	721	ADIVSSLRMACTCCIS KLENLAMILIDKDAWNKEEFSVLD EFTRSKVTFTTRVPKIFLLA	780	
Db	872	ADIVSSLRMACTCCIS KLENLAMILIDKDAWNKEEFSVLD EFTRSKVTFTTRVPKIFLLA	931	
QY	781	TSATLTERSEMKSTGLIDEVVIKPLRMSVLI CCLOETLVNGKKRQPNRQRRLGHLIREK	840	
Db	932	TSATLTERSEMKSTGLIDEVVIKPLRMSVLI CCLOETLVNGKKRQPNRQRRLGHLIREK	991	
QY	841	QILVVDDNLVNR RVAEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF	900	
Db	992	QILVVDDNLVNR RVAEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF	1051	
QY	901	EATRRVRELEREINKKIASGEVSAEMFC FSSWHVPILAMTADVIQATHEECMKCGMDGY	960	
Db	1052	EATRRVRELEREINKKIASGEVSAEMFC FSSWHVPILAMTADVIQATHEECMKCGMDGY	1111	
QY	961	VSKPFE EEVLYTAVARFF EPC	981	
Db	1112	VSKPFE EEVLYTAVARFF EPC	1132	
RESULT 2				
AAG47089				
ID	AAG47089 standard; Protein; 1176 AA.			
XX				
AC	AAG47089;			
XX				
DT	18-OCT-2000 (first entry)			
XX				
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 59313.			
XX				
KW	Protein identification; signal transduction pathway; metabolic pathway;			
KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KW	termination sequence.			
XX				
OS	Arabidopsis thaliana.			
XX				
PN	EP1033405-A2.			
XX				
PD	06-SEP-2000.			
XX				
PF	25-FEB-2000; 2000EP-0301439.			
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PR	25-FEB-1999; 99US-0121825.			
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PR	29-MAR-1999; 99US-0126785.			
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
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PR 06-AUG-1999; 99US-0147303.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.

CC	presented is the A. thaliana cytokinin receptor, AHK2, protein.									
XX										
SQ	Sequence	1176 AA;								
	Query Match	100.0%;	Score	5019;	DB	23;	Length	1176;		
	Best Local Similarity	100.0%;	Pred. No.	0;						
	Matches	981;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	KARGERKEKVLQ	EALAPKQQQAQTSSRGAGRWKNI	LLGILGGVSFV	WFWDTNE	60				
Db	196	KARGERKEKVLQ	EALAPKQQQAQTSSRGAGRWKNI	LLGILGGVSFV	WFWDTNE	255				
QY	61	EIIMKRRETLAN	CDERARVLQDFNVSLNHVHALSILVSTFHHGKI	PSAIDQRTFE	EYTT	120				
Db	256	EIIMKRRETLAN	CDERARVLQDFNVSLNHVHALSILVSTFHHGKI	PSAIDQRTFE	EYTT	315				
QY	121	ERTNFERPLTSG	VAYALKVPHSEREKFEKEHGAIAKKMETEDQTVVQDCVP	ENFDPAPIQ	180					
Db	316	ERTNFERPLTSG	VAYALKVPHSEREKFEKEHGAIAKKMETEDQTVVQDCVP	ENFDPAPIQ	375					
QY	181	DEYAPVIFAQET	VSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNH	LGVLT	240					
Db	376	DEYAPVIFAQET	VSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNH	LGVLT	435					
QY	241	AVYDTSLPPDATE	EQRVEATIGYLGASYDNPSLVEKLLHQLASKQTI	AVDVYDTTNTSGL	300					
Db	436	AVYDTSLPPDATE	EQRVEATIGYLGASYDNPSLVEKLLHQLASKQTI	AVDVYDTTNTSGL	495					
QY	301	IKMYGSEIGDIS	EQHISSLDFGDPSPRNHEMHCRFKHLPIPWTAITPSILVLVIT	FLVG	360					
Db	496	IKMYGSEIGDIS	EQHISSLDFGDPSPRNHEMHCRFKHLPIPWTAITPSILVLVIT	FLVG	555					
QY	361	ILYEAINRIATV	EEDCQKRELKARAEADIAKSQFLATVSHEIRTPMNGVLGMLK	MLMD	420					
Db	556	ILYEAINRIATV	EEDCQKRELKARAEADIAKSQFLATVSHEIRTPMNGVLGMLK	MLMD	615					
QY	421	TDLDAKQMDYAT	AGSGKDLTSLINEVLDAQIESGRLELENVPDMRFILDNV	SLLS	480					
Db	616	TDLDAKQMDYAT	AGSGKDLTSLINEVLDAQIESGRLELENVPDMRFILDNV	SLLS	675					
QY	481	GKANEKGIELAV	VSSQVPDVVGDPSPRFRQIITNLVNSIKFTQERGHIFISV	HLADEV	540					
Db	676	GKANEKGIELAV	VSSQVPDVVGDPSPRFRQIITNLVNSIKFTQERGHIFISV	HLADEV	735					
QY	541	KEPLTIEDAVLK	QRLALGCSEGETVSGFPANAWGSKNFKTCYSTESQNSDQ	IKLLVT	600					
Db	736	KEPLTIEDAVLK	QRLALGCSEGETVSGFPANAWGSKNFKTCYSTESQNSDQ	IKLLVT	795					
QY	601	VEDTGVGIPVDA	QGRIFTFPMQADSSSTRYGGTGIGLSISKRLVELMQGEMGF	VSEPGI	660					
Db	796	VEDTGVGIPVDA	QGRIFTFPMQADSSSTRYGGTGIGLSISKRLVELMQGEMGF	VSEPGI	855					
QY	661	GSTFSFTGVFG	KAEINTSITKLERFDLAIQFETGLRALVIDNRNIRAEVTRY	ELRRLGIS	720					
Db	856	GSTFSFTGVFG	KAEINTSITKLERFDLAIQFETGLRALVIDNRNIRAEVTRY	ELRRLGIS	915					
QY	721	ADIVSSLRMACT	CCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFT	TRVPKIFLLA	780					
Db	916	ADIVSSLRMACT	CCISKLENLAMILIDKDAWNKEEFSVLDELFTRSKVTFT	TRVPKIFLLA	975					
QY	781	TSATLTERSEMK	STGLIDEVWIKPLRMSVLICLQETLVNGKKRQPNRNLGH	LRLREK	840					
Db	976	TSATLTERSEMK	STGLIDEVWIKPLRMSVLICLQETLVNGKKRQPNRNLGH	LRLREK	1035					
QY	841	QILVDDNLVNR	RVAEGALKKYGAIVTCVESGKAALAMLKPPHNFACFMD	LQMPMDGF	900					
Db	1036	QILVDDNLVNR	RVAEGALKKYGAIVTCVESGKAALAMLKPPHNFACFMD	LQMPMDGF	1095					
QY	901	EATRRVRELER	INKKIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEE	CMCGMDGY	960					
Db	1096	EATRRVRELER	INKKIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEE	CMCGMDGY	1155					
QY	961	VSKPFEFEEV	LYTAVARFFPC	981						

Db	1156	VSKPFEFEEVLYTAVARFFPC	1176										
RESULT 4													
AAE33692													
ID	AAE33692	standard; Protein; 1176 AA.											
XX	AC												
XX	AAE33692;												
DT	16-APR-2003	(first entry)											
XX													
DE	Arabidopsis thaliana histidine kinase 2 (AHK2) protein.												
XX													
KW	Shoot formation; senescence; transgenic; transgenic plant; agriculture;												
KW	cell proliferation; shoot meristem formation; leaf development; AHK;												
KW	photosynthesis; histidine kinase; enzyme.												
XX													
OS	Arabidopsis thaliana.												
XX													
PN	WO200299079-A2.												
XX													
PD	12-DEC-2002.												
XX													
PF	06-JUN-2002; 2002WO-US18066.												
XX													
PR	06-JUN-2001; 2001US-296554P.												
XX													
PA	(GEHO) GEN HOSPITAL CORP.												
XX													
PI	Sheen J, Hwang I;												
XX													
WPI	2003-140613/13.												
DR	N-PSDB; AAD51604.												
DR													
XX													
PT	Increasing yield in plant, increasing shoot formation in a plant, or												
PT	delaying senescence in a plant such as wheat, rice, maize, barley,												
PT	potato, by using transgenes that regulate cytokinin response -												
XX													
PS	Disclosure; Page 75-78; 87pp; English.												
XX													
CC	The present invention relates to a novel method of increasing yield in a												
CC	plant, increasing shoot formation or delaying senescence in a plant. The												
CC	method involves introducing into plant cells, a transgene having a B-type												
CC	response regulator operably linked to a promoter functional in plant												
CC	cells to yield transformed plant cells or whose expression reduces the												
CC	expression of A-type response regulator in the cells of the plant and												
CC	regenerating a plant from the transformed cells. The method is useful												
CC	for increasing the yield in a plant, increasing the shoot formation or												
CC	delaying senescence in a plant such as wheat, rice, maize, barley,												
CC	potato, tomato, soybean, oat, cotton and sunflower. The method												
CC	is useful for variety of agricultural and commercial purposes including												
CC	improving and enhancing photosynthesis, promoting cell proliferation,												
CC	shoot meristem formation, promoting leaf development, increasing crop												
CC	yields, improving crop and ornamental quality and reducing agricultural												
CC	production costs. The present sequence is Arabidopsis thaliana histidine												
CC	kinase 2 (AHK2) protein. This sequence is used to illustrate the method												
CC	of the invention.												
XX													
SQ	Sequence	1176 AA;											
Query Match													
Best Local Similarity 100.0%; Score 5019; DB 24; Length 1176;													
Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;													
QY	1	KARGERKEKVLQ	EALAPKQQQAQTSSRGAGRWKNI	LLGILGGVSFV	WFWDTNE	60							
Db	196	KARGERKEKVLQ	EALAPKQQQAQTSSRGAGRWKNI	LLGILGGVSFV	WFWDTNE	255							
QY	61	EIIMKRRETLAN	CDERARVLQDFNVSLNHVHALSILVSTFHHGKIP	SAIDQRTFE	EYTT	120							
Db	256	EIIMKRRETLAN	CDERARVLQDFNVSLNHVHALSILVSTFHHGKIP	SAIDQRTFE	EYTT	315							

PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.

PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 5019; DB 21; Length 1238;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 981; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KARGERKEKVHLOEALAPKKQQQRAQTSSRGAGRWRKNILLGILGGVSFVWFWDTNE 60
Db 258 KARGERKEKVHLOEALAPKKQQQRAQTSSRGAGRWRKNILLGILGGVSFVWFWDTNE 317
QY 61 EIIMKRRETLANMCDERARVLQDQFNVSNLNVHVALSILVSTFHHGKIPSAIDORTFEEYT 120
Db 318 EIIMKRRETLANMCDERARVLQDQFNVSNLNVHVALSILVSTFHHGKIPSAIDORTFEEYT 377
QY 121 ERTNFERPLTSGVAYALKVPHSREKFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 180
Db 378 ERTNFERPLTSGVAYALKVPHSREKFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 437
QY 181 DEYAPVIFAQETVSHIVSVDMMSGEEDRENILRARASGKGVLTSPFKLLKSNHLGVVLTTF 240
Db 438 DEYAPVIFAQETVSHIVSVDMMSGEEDRENILRARASGKGVLTSPFKLLKSNHLGVVLTTF 497
QY 241 AVYDTSLPDPDATEEQRVEATIGYGASYDMPSLVEKLLHQLASKQTIADVVDYDTTNTSGL 300
Db 498 AVYDTSLPDPDATEEQRVEATIGYGASYDMPSLVEKLLHQLASKQTIADVVDYDTTNTSGL 557
QY 301 IKMYGSEIGDISEQHISSLDFGDPSPSRNHMHCRFKHKLPWPWTAITPSILVLVITFLVG 360
Db 558 IKMYGSEIGDISEQHISSLDFGDPSPSRNHMHCRFKHKLPWPWTAITPSILVLVITFLVG 617

QY 361 ILYEAINRIATVEEDCQKRELKARAEAAIAKSOPLATVSHEIRTPMNGVLGMLKMLMD 420
|||
Db 618 ILYEAINRIATVEEDCQKRELKARAEAAIAKSOPLATVSHEIRTPMNGVLGMLKMLMD 677
QY 421 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFILDNVSSLLS 480
|||
Db 678 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFILDNVSSLLS 737
QY 481 GKANEKGIELAVYVSSQVDDVVGDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
|||
Db 738 GKANEKGIELAVYVSSQVDDVVGDPSRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 797
QY 541 KEPLTIEDAVLKQRLALGCSSEGETVSGFPAVNAWGSWKNFKTCYSTESQSDQIKLLVT 600
|||
Db 798 KEPLTIEDAVLKQRLALGCSSEGETVSGFPAVNAWGSWKNFKTCYSTESQSDQIKLLVT 857
QY 601 VEDTGVGIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 660
|||
Db 858 VEDTGVGIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 917
QY 661 GSTFSFTGVFGKAETNTSITKLERFDLAIQFTGLRALVIDNRNIRAEVTRYELRRLGIS 720
|||
Db 918 GSTFSFTGVFGKAETNTSITKLERFDLAIQFTGLRALVIDNRNIRAEVTRYELRRLGIS 977
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDLFTRSKVTFTRPVKIFLLA 780
|||
Db 978 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDLFTRSKVTFTRPVKIFLLA 1037
QY 781 TSATLTERSEMKTGLIDEVVIKPLRMSVLI CCLQETLVNGKKRQPNRQRLGHLLEK 840
|||
Db 1038 TSATLTERSEMKTGLIDEVVIKPLRMSVLI CCLQETLVNGKKRQPNRQRLGHLLEK 1097
QY 841 QILVDDNLVNRRAEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 900
|||
Db 1098 QILVDDNLVNRRAEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 1157
QY 901 EATRRVRELEREINKKIASGEVSAEMFCFSSWHVPILAMTADVIQATHEECMKCGMDGY 960
|||
Db 1158 EATRRVRELEREINKKIASGEVSAEMFCFSSWHVPILAMTADVIQATHEECMKCGMDGY 1217
QY 961 VSKPFEVEVLYTAVARFFEP C 981
|||
Db 1218 VSKPFEVEVLYTAVARFFEP C 1238

RESULT 6
ID AAO22568 standard; Protein; 1173 AA.
XX
AC AAO22568;
DT 28-OCT-2002 (first entry)
XX
DE Wooden leg (WOL) gene related protein SEQ ID No 19.
XX
KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.
XX
OS Arabidopsis thaliana.
XX
PN WO200244337-A2.
XX
PD 06-JUN-2002.
XX
PF 29-NOV-2001; 2001WO-US45053.
XX
PR 29-NOV-2000; 2000US-253739P.
XX
PA (UJNY) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.

PA (RIIK/) RIIKONEN M.
XX
PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;
XX
DR WPI; 2002-599423/64.
XX
PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants -
XX
PS Example 1; Page 161-164; 187pp; English.
XX
CC The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
CC comprising 15 contiguous amino acids of a fully defined Arabidopsis
CC WOODEN LEG protein sequence of 1057 amino acids as given in the
CC specification, and to its encoding nucleic acid. The invention also
CC relates to an amino acid sequence of domains of protein, e.g., N-terminal
CC region, C-terminal domain, etc; or is a naturally occurring allelic
CC variant of the above mentioned polypeptide sequence. Expression levels of
CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of
CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.
XX
SQ Sequence 1173 AA;

Query Match 99.5%; Score 4991.5; DB 23; Length 1173;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 978; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 KARGERKEKVLQAEALAPKKQQRAQTSSRGAGRWKRNILLGILGVSFSVWFWDTNE 60
|||
Db 196 KARGERKEKVLQAEALAPKKQQRAQTSSRGAGRWKRNILLGILGVSFSVWFWDTNE 255
QY 61 EIIMKRRETLANMCDERARVLQDQFNVSINHVHALSILVSTFHHGKIPSAIDQRTFEY 120
|||
Db 256 EIIMKRRETLANMCDERARVLQDQFNVSINHVHALSILVSTFHHGKIPSAIDQRTFEY 315
QY 121 ERTNFERPLTSGVAYALKVPHSEREKEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 180
|||
Db 316 ERTNFERPLTSGVAYALKVPHSEREKEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 375
QY 181 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHGLGVLT 240
|||
Db 376 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHGLGVLT 435
QY 241 AVYDTSLPDPDATEEQRVEATIGYLGSYDMPSPSLVEKLLHQLASKQTIAVDVYDTTNTSGL 300
|||
Db 436 AVYDTSLPDPDATEEQRVEATIGYLGSYDMPSPSLVEKLLHQLASKQTIAVDVYDTTNTSGL 495
QY 301 IKMYGSEIGDISEQHISSLDGDPDRNHEMHCRFKHKLPIPWTAITPSILVLVITFLVGY 360
|||
Db 496 IKMYGSEIGDISEQHISSLDGDPDRNHEMHCRFKHKLPIPWTAITPSILVLVITFLVGY 555
QY 361 ILYEAINRIATVEEDCQKRELKARAEAAIAKSOFLATVSHEIRTPMNGVLGMLKMLMD 420
|||
Db 556 ILYEAINRIATVEEDCQKRELKARAEAAIAKSOFLATVSHEIRTPMNGVLGMLKMLMD 615
QY 421 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVPFDMRFILDNVSSLLS 480

Db 616 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVDFMRFILDNVSSLLS 675
QY 481 GKANEGIELAVYVSSQVDDVVVGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 676 GKANEGIELAVYVSSQVDDVVVGDPSPRFRQIITNLVGNISIK---ERGHIFISVHLADEV 732
QY 541 KEPLTIEDAVLKQRLALGCSEGETVSGFPAVNAWGSWKNFKTCYSTESQNSDQIKLLVT 600
Db 733 KEPLTIEDAVLKQRLALGCSEGETVSGFPAVNAWGSWKNFKTCYSTESQNSDQIKLLVT 792
QY 601 VEDTGVGIPVDAQGRIFTPEMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 660
Db 793 VEDTGVGIPVDAQGRIFTPEMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 852
QY 661 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAEVTRYELRRLGIS 720
Db 853 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAEVTRYELRRLGIS 912
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTTRSKVTFTRVPKIFLLA 780
Db 913 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTTRSKVTFTRVPKIFLLA 972
QY 781 TSATLTERSEMKTGLIDEVWIKPLRMSVLICCLQETLVNGKKRQPNRQRRNLGHLREK 840
Db 973 TSATLTERSEMKTGLIDEVWIKPLRMSVLICCLQETLVNGKKRQPNRQRRNLGHLREK 1032
QY 841 QILVVDDNLVNRVAEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 900
Db 1033 QILVVDDNLVNRVAEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGF 1092
QY 901 EATRRVRELERHINKKIASGEVSAEMFCFSSWHVPILAMTADVIQATHEECMKGMDGY 960
Db 1093 EATRRVRELERHINKKIASGEVSAEMFCFSSWHVPILAMTADVIQATHEECMKGMDGY 1152
QY 961 VSKPFEEVLYTAVARFFEP 981
Db 1153 VSKPFEEVLYTAVARFFEP 1173

RESULT 7
ABB93625
ID ABB93625 standard; Protein; 1173 AA.
XX
AC ABB93625;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 2836.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.
XX
(FARB) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX

Ps Claim 5; SEQ ID NO 2836; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 1173 AA;
Query Match 99.5%; Score 4991.5; DB 23; Length 1173;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 978; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 KARGERKEKVLQEQALAPKKQOQRAQTSSRGAGRWKRNILLGILGGVSFVWFWDTNE 60
Db 196 KARGERKEKVLQEQALAPKKQOQRAQTSSRGAGRWKRNILLGILGGVSFVWFWDTNE 255
QY 61 EIIMKRRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHHGKIPSAIDQRTFEEYT 120
Db 256 EIIMKRRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHHGKIPSAIDQRTFEEYT 315
QY 121 ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 180
Db 316 ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 375
QY 181 DEVAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHLGVVLT 240
Db 376 DEVAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKGLTSPFKLLKSNHLGVVLT 435
QY 241 AVYDTSLPDATEEQRVEATIGYLGASYDMPSLVEKLHLQASKQTIADVVDYDTTNTSGL 300
Db 436 AVYDTSLPDATEEQRVEATIGYLGASYDMPSLVEKLHLQASKQTIADVVDYDTTNTSGL 495
QY 301 IKMYGSEIGDISEQHISSLDFGDPSPRNHEMHCRFKHKLPWPWTAITPSILVLVITFLVGY 360
Db 496 IKMYGSEIGDISEQHISSLDFGDPSPRNHEMHCRFKHKLPWPWTAITPSILVLVITFLVGY 555
QY 361 ILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSHEIRTPMNGVLGMLKMLMD 420
Db 556 ILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSHEIRTPMNGVLGMLKMLMD 615
QY 421 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVDFMRFILDNVSSLLS 480
Db 616 TDLDAKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVDFMRFILDNVSSLLS 675
QY 481 GKANEGIELAVYVSSQVDDVVVGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 676 GKANEGIELAVYVSSQVDDVVVGDPSPRFRQIITNLVGNISIK---ERGHIFISVHLADEV 732
QY 541 KEPLTIEDAVLKQRLALGCSEGETVSGFPAVNAWGSWKNFKTCYSTESQNSDQIKLLVT 600
Db 733 KEPLTIEDAVLKQRLALGCSEGETVSGFPAVNAWGSWKNFKTCYSTESQNSDQIKLLVT 792
QY 601 VEDTGVGIPVDAQGRIFTPEMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 660
Db 793 VEDTGVGIPVDAQGRIFTPEMQADSSSTRTYGGTGIGLSISKRLVELMQGEMGFVSEPGI 852
QY 661 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAEVTRYELRRLGIS 720
Db 853 GSTFSFTGVFGKAETNTSITKLERFDLAIQEBFTGLRALVIDNRNIRAEVTRYELRRLGIS 912
QY 721 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTTRSKVTFTRVPKIFLLA 780
Db 913 ADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTTRSKVTFTRVPKIFLLA 972
QY 781 TSATLTERSEMKTGLIDEVWIKPLRMSVLICCLQETLVNGKKRQPNRQRRNLGHLREK 840
Db 973 TSATLTERSEMKTGLIDEVWIKPLRMSVLICCLQETLVNGKKRQPNRQRRNLGHLREK 1032

QY	841	QILVDDNLVNR	VAEGALKKYG	AI	VT	CVESGKA	ALAM	LKPPH	NF	DACF	MDLQ	MP	MDG	900		
D	b	1033	QILVDDNLVNR	VAEGALKKYG	AI	VT	CVESGKA	ALAM	LKPPH	NF	DACF	MDLQ	MP	MDG	1092	
QY	901	EATRRVRE	LEREIN	KKIAS	GEVSA	EMFCK	FSSWH	VPIL	AMTAD	VI	QATHEE	CMK	CG	MDY	960	
D	b	1093	EATRRVRE	LEREIN	KKIAS	GEVSA	EMFCK	FSSWH	VPIL	AMTAD	VI	QATHEE	CMK	CG	MDY	1152
QY	961	VSKPFE	EEVLYT	AVAR	FF	EP	C	981								
D	b	1153	VSKPFE	EEVLYT	AVAR	FF	EP	C	1173							

RESULT 8

ABG70782	
ID	ABG70782 standard; Protein; 1036 AA.
XX	
XX	
AC	ABG70782;
XX	
DT	09-DEC-2002 (first entry)
XX	
DE	A. thaliana cytokinin receptor, AHK3, protein.
XX	
KW	AHK3; plant; antagonist; agonist; cytokinin receptor;
KW	receptor; signal transduction; histidine kinase; hormone; cell division;
KW	cell differentiation; agriculture; growth regulator; harvest.
XX	
OS	Arabidopsis thaliana.
XX	
FH	Key
FT	Location/Qualifiers
FT	32..1036
FT	/note= "This region is specifically claimed in Claim 1"
XX	
PN	EP1241182-A2.
XX	
PD	18-SEP-2002.
XX	
PF	13-MAR-2002; 2002EP-0005749.
XX	
PR	15-MAR-2001; 2001JP-0073812.
PR	29-JUN-2001; 2001JP-0198639.
PR	29-JUN-2001; 2001JP-0198640.

(SUMO) SUMITOMO CHEM CO LTD.

Kakimoto T, Higuchi M, Inoue T;

WPI; 2002-693041/75.

N-PSDB; ABS54451.

Analyzing agonist or antagonist activity of a substance for use as a plant growth regulator, comprises measuring intracellular signal transduction from a cytokinin receptor expressed in a cell contacted with the test substance -

Claim 1; Page 32-34; 47pp; English.

The invention discloses a method for analysing antagonist or agonist activity to a cytokinin receptor. The method comprises bringing a candidate substance into contact with a transformed cell, in which a DNA encoding the receptor has been introduced, and then measuring the existence, or the quantity, of the intracellular signal transduction from the receptor expressed in the cell. The cytokinin receptor comprises an extracellular region of the receptor, transmembrane regions, a histidine kinase region and a receiver region of the kinase. The transmembrane regions and kinase region are homogeneous to each other and the receptor region is heterogeneous to them. Cytokinins are plant hormones relevant to cell division and differentiation of higher plants. The method is used for analysing agonist or antagonist activity to a cytokine receptor. A substance with agonist or antagonist activity to the receptor can be used, in agriculture, as a plant growth regulator, e.g. after harvest. The advantage is that the candidate substances do not need to be prepared.

KW Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.
XX Arabidopsis thaliana.
OS WO200244337-A2.
XX 06-JUN-2002.
XX 29-NOV-2001; 2001WO-US45053.
XX 29-NOV-2000; 2000US-253739P.
PA (UJNY) UNIV NEW YORK STATE.
PA (HELA/) HELARIUTTA Y.
PA (MAHO/) MAHONEN A P.
PA (BONK/) BONKE A W M.
PA (KAUP/) KAUPPINEN L.
PA (RIIK/) RIIKONEN M.
XX Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;
XX WPI; 2002-599423/64.
PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants -
XX
PS Example 1; Page 157-161; 187pp; English.
XX The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
CC comprising 15 contiguous amino acids of a fully defined Arabidopsis
CC WOODEN LEG protein sequence of 1057 amino acids as given in the
CC specification, and to its encoding nucleic acid. The invention also
CC relates to an amino acid sequence of domains of protein, e.g., N-terminal
CC region, C-terminal domain, etc; or is a naturally occurring allelic
CC variant of the above mentioned polypeptide sequence. Expression levels of
CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of
CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.
XX
SQ Sequence 1092 AA;

Query Match 51.7%; Score 2595.5; DB 23; Length 1092;
Best Local Similarity 55.0%; Pred. No. 1.1e-217;
Matches 538; Conservative 141; Mismatches 220; Indels 79; Gaps 14;

QY 35 WRKNILLGILGVSFVWVFWDTNNEIIMKXRETLANCMCDERARVLQDFNVSLNHVHA 94
Db 92 WRK-LVVVWVFWVLVSIWTFWYFSSQAMEKXKETLASMCDERARMLQDFNVSMNHVQA 150
QY 95 LSILVSTFHHGKIPSAIDQRTFEEYTERTFNFERPLTSGVAYALKVPHSEREKFEKEHGW 154
Db 151 MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEFEFERQOGWT 210
QY 155 IKKMETEDQTVV--QDCVPENFDPAIQDEYAPVIFAQETVSHVSDVMSGEEDRENIL 212
Db 211 IRKMYSLQNPNVHKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVSVSLDMLSGKEDRENVL 270

QY 213 RARASGKGLTSPFKLLKSNHLGVLTFAVYDTSLPPDATEEQRVEATIGYLGASYDMP 272
Db 271 RARSSGKGLTAPFPPLIKTNRLGVILTFAVYKRDLPNSATPKERIEATNGYLGVDIES 330
QY 273 LVEKLHLQASKQTIADVVDYDTNTSGGLIKMYGSEIGDISEQHSSLDGDPSPRNHEMH- 331
Db 331 LVENLLQQLASKQTIILVNVYDITNHSQPISMYGTNVSDAGLERSPLIFGDLRKHMER 390
QY 332 -----CRFKHKLPIPWTAITPSILVLVITFLVGY 360
Db 391 RYLQLAHTYVCNFFLFARIQVLTFCCELLPLCRFKQKPPWPVLSMVTSEGILVIALLV 450
QY 361 ILYEAINRIATVEEDCQKMRLEKARAEAAIAKQFLATVSHHRTPMNGVLGMLKMLMD 420
Db 451 IIHATVSRHKKVEEDCDKMKQLKKKAEAADVAKSQFLATVSHHRTPMNGVLGMLHMLMD 510
QY 421 TDLDKQMDYAQTAHSGKDLTSLINEVLDQAKIESGRLELENVFPDMRFILDNVSSLLS 480
Db 511 TELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLELEVRFDLRGILDVLSLFS 570
QY 481 GKANEKGLIELAVYVSSQVDPVVVGDPSPFRFQIITNLVGNISIKFTQERGHIFISVHLADEV 540
Db 571 SKSQKGVELAVYISDRVPDMLIGDPGRFRQILTNLMGNSIKFT-EKGHIFVTVHLVDEL 629
QY 541 KEPLTIHDAVLKQRLALGCSEGETVSGFPVAVNAWGSWKNFKTCYSTESQNS-----DQI 595
Db 630 FESIDGETA-----SSPESTLSGLPVADRQRSWENFK-APSSNGHRSFEPSPPDI 678
QY 596 KLLVTVEDTGVGIPVDAQGRIFTPEMQADSSSTRTYGGTGIGLISIKRLVELMQGEMGFV 655
Db 679 NLIVSVEDTGVGIPVEAQSRIFTPEMQVGPISIRTHGGTGIGLISIKCLVGLMKGEIGFS 738
QY 656 SEPGIGSTFSFTGVFG-----KAETNTSITKLERFDLAIQFTGLRALVIDNRNIRA 707
Db 739 STPKVGSTFTTAVFSNGMQPAERKNDNNQPI-----FSEFRGMKAVVVDHRPARA 789
QY 708 EVTRYELRRLGISADIVSSLRMACTCCISKLENLAMILIDKDAWNKEEFSVLDELFTRSK 767
Db 790 KVSWHFQRLGIRVEVVRVEQALHYLKIGTTTNNMILIEQEIWNREADDFIKKL---QK 846
QY 768 VTFTRVPKIFLLATSATLTERSEMKGSTGLIDE--VVIKPLRMSVLICLQETLVNGKKRQ 825
Db 847 DPLFLSPKILLANSVE-SSISEALCTG-IDPPIVIVKPLRASMLAATLQRLGIGIREP 904
QY 826 PNRQ---RRNLGHLRLREKQILVDDNLVNRRAEGALKKYGAIVTCVESGKAALAMLKPP 882
Db 905 PQHKGPPALILRNLLGRKILIVDDNNVNLVRAAGALKKYGADVCAESGIIKAI SLLKPP 964
QY 883 HNFDAFMDLQMPMDGFEATRRVRELEEREINKKIASGEVSAEMFCKFSSWHVPILAMTA 942
Db 965 HEFDACFMDIQMPMDGFEATRRIRIRDMEEEMNKRIKNGEALIVNGNKTSWHLPLVAMTA 1024
QY 943 DVIQATHEECMKCGMDGY 960
Db 1025 DVIQATHEECLKCGMDGY 1042

RESULT 11
ABB91150
ID ABB91150 standard; Protein; 1092 AA.
XX
AC ABB91150;
XX
DT 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 361.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.

CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.
XX
SQ Sequence 1057 AA;

Query Match 50.6%; Score 2539.5; DB 23; Length 1057;
Best Local Similarity 53.2%; Pred. No. 8.4e-213;
Matches 537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;

QY 4 GERKEKVLQE--ALAPKKQQQRAQTSSRGAGRWKKNILLGILGGVSFSVW-WFWDPTNE 60
Db 89 GNKKGSTFIQEHRA LLPKAL-----ILWIIIVGFISSGIYQWMDANK 131
QY 61 EIIMKRETLANCMDERARVLQDFNVSLNHVHALSILVSTFHGKIPSAIDQRTFEHYT 120
Db 132 ---IRREVLVSMCDQARMLQDFSVNVHVHALAILVSFHYHKNPISAIDQETFAEY 188
QY 121 ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 180
Db 189 ARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTM-----DRGEPSVVR 235
QY 181 DEYAPVIFAQETVSHIVSVDMMSGEEDRENILRARASGKGLTSPFKLLKSNHLGVVLT 240
Db 236 DEYAPVIFSQDSVSYLESLESDMMSGEEDRENILRARETGKAVLTSPFRLLLETHLGVVLT 295
QY 241 AVYDTSLPDATEEQRVEATIGYLGASYDMPSLVEKLLHQLASKQTIADVVDYDTTNTSGL 300
Db 296 PVYKSLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNQAIVVHVYDITNASDP 355
QY 301 IKMYGS--EIGDISEQHISSLDFGSPSRNHMHCRFKHKLPWPWTAITPSILVLVITFLV 358
Db 356 LVMYGNQDEEADRSLSHESKLDGDFPRKHKMICRYHQKAPIPLNLTTPVPLFAIGFLV 415
QY 359 GYILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSHEIRTPMNGVLGMLKML 418
Db 416 GYILYGAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAML 475
QY 419 MDTDLDAKQMDYAQTAHGSGKDLTSLINEVLDAQIESGRLELENVPFDMRFIELDNVSSL 478
Db 476 LDTELSSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVL 535
QY 479 LSGKANKEGIELAVYSSQVPDVVGDPSRFRQIITNLVGNISIKFTQERGHIFISVHLAD 538
Db 536 FSEESRNKSIELAVFVSDKVPEIVKGDPSGRFRQIIINLVGNSVKFT-EKGHIFVKVHLAE 594
QY 539 EVK---EPL-TIEDAVLKQRLALGCSBSGETVSGFPVAVNANGSWKNFKTCYSTESQNSD- 593
Db 595 QSKDESEPKNALGGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSPFKHLVSEEQSLSEF 654
QY 594 ----QIKLVTVTEDTGVGIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQ 649
Db 655 DISSNVRLMVSIEDTGIGIPLVAQGRVPMFPMQADSSSTRNYGGTGIGLSISKCLVELMR 714
QY 650 GEMGFVSEPGIGSTFSFTGVFGKAETNITSITKLER--FDLAIQEFTGLRALVIDNRNIRA 707
Db 715 GQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAIVVDKPVRA 774
QY 708 EVTRYELRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKDAW-----NK 753
Db 775 AVTRYHMKRLGINVDVVTSLKTAVVAAAAAFERNGPSLPTKPQLDMILVEKDSWISTEDND 834
QY 754 EEFSVLDELFTRSKVTFTFRVPKIFLLATSATLTERSEMKSTGLIDEVVIKPLRMSVLICC 813

Db 835 SEIRLLNSR-TNGNV-HHKSPKALAFATNITNSEEDRAKSAGFADTVIMKPLRASMIGAC 892
QY 814 LQETLVNGKKRQPNRQRN---LGHLLREKQILVVDDNLVNRRAEGALKKYCAIVTCVE 870
Db 893 LQQVLELRKTRQQHPGSSPATLKSLLTGKKILVVDDNIVNRRVAAGALKKFGAEVVCAE 952
QY 871 SGKAALAMLKPPHNFDFACFMDLQMPMDGFQATRRVRELEREINKKIASGEVSAEMFCKF 930
Db 953 SGQVALGLLQIPHTFDACFMDIQMPQMDGFQATRRVRELEREINKKIASGEVSAEMFCKF 1000
QY 931 SSWHVPILAMTADVIOATHEECMKCGMDGYVSKPFEEVLYTAVARFFEP 980
Db 1001 LEWHLPILAMTADVIHATYEECLKSGMDGYVSKPFEEENLYKSVAKSFKP 1050

RESULT 14

AAO22570

ID AAO22570 standard; Protein; 1057 AA.

XX AAO22570;

DT 28-OCT-2002 (first entry)

DE Wooden leg (WOL) gene related protein SEQ ID No 24.

XX Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.

XX Arabidopsis thaliana.

PN WO200244337-A2.

PD 06-JUN-2002.

XX 29-NOV-2001; 2001WO-US45053.

XX 29-NOV-2000; 2000US-253739P.

XX (UUNY) UNIV NEW YORK STATE.

PA (HELA/) HELARIUTTA Y.

PA (MAHO/) MAHONEN A P.

PA (BONK/) BONKE A W M.

PA (KAUP/) KAUPPINEN L.

PA (RIIK/) RIIKONEN M.

XX Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;

PI Benfey PN;

XX WPI; 2002-599423/64.

PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set

PT of asymmetric cell divisions that establish vascular tissue in root and

PT hypocotyl development, useful for improving agronomically valuable

PT plants -

XX Disclosure; Page 167-171; 187pp; English.

CC The invention relates to an isolated WOODEN LEG (WOL) polypeptide,

CC comprising 15 contiguous amino acids of a fully defined Arabidopsis

CC WOODEN LEG protein sequence of 1057 amino acids as given in the

CC specification, and to its encoding nucleic acid. The invention also

CC relates to an amino acid sequence of domains of protein, e.g., N-terminal

CC region, C-terminal domain, etc; or is a naturally occurring allelic

CC variant of the above mentioned polypeptide sequence. Expression levels of
CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of
CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products

CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.
XX
SQ Sequence 1057 AA;

Query Match 50.6%; Score 2539.5; DB 23; Length 1057;
Best Local Similarity 53.2%; Pred. No. 8.4e-213;
Matches 537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;

QY 4 GERKEKVLQE--ALAPKKQQQRAQTSSRGAGRWKRNILLGILGVSFVW-WFWDTNE 60
Db 89 GNKKGSTFIQEHRAALLPKAL-----ILWIIIVGFISSGIQWMDANK 131
QY 61 EIIMKRRETLANCMDERARVLQDQFNVSLSNHVHALSTLVTFHHGKIPSAIDQTFEEYT 120
Db 132 ---IRREEVLVSMCDQARMQLQDQFSVSNHVHALAILVSTFHYHKNPNSAIDQETFAEYT 188
QY 121 ERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKGMETEDQTVVQDCVPENFDPAPIQ 180
Db 189 ARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTM-----DRGEPSPVR 235
QY 181 DEYAPVIFAQETVSHIVSDMMSGEEDRENILRASGKGVLTSPFKLLKSNHLGVWLTF 240
Db 236 DEYAPVIFSQDSVSYLESMDMSGEEDRENILRARETGKAVLTSPFRLLLETHLGVWLTF 295
QY 241 AVYDTSLPPDATEEQRVETATIGYLGASYDMPSLVEKLLHQLASKQTIADVVDYDTNTSGL 300
Db 296 PVYKSSLPENPTVEERIAATAGYLGGAFDVESLVENLLGQLAGNAIVVHVYDITNASDP 355
QY 301 IKMYGS--EIGDISEQHISLDFGDPSPRNHEMHCFFKHKLPIPTAITPSILVIVITFLV 358
Db 356 LVMYGNQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTVLFFAIGFLV 415
QY 359 GYILYEAINRIATVEEDCQKRELKARAEAAIAKSQFLATVSHSHEIRTPMNGVLGMLKML 418
Db 416 GYILYGAAHVIKVEDDFHEMQELKVRAEAAVAKSQFLATVSHSHEIRTPMNGILGMLAML 475
QY 419 MDTDLDAKQMDYAQTAHSGGKDLTSLINEVLDQAKIESGRLELENVPFDMRFILDNVSSL 478
Db 476 LDTELSSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSL 535
QY 479 LSGKANEGIELAVYVSSQVPDVVVGDPSPRFRQITNLVGNISIKFTQERGHIFISVHLAD 538
Db 536 FSEESRNKSIELAVFVSDKVPKIEVKGDSGRFRQIINLVGNSVKFT-EKGHIFVKVHLAE 594
QY 539 EVK---EPL-TIEDAVLKQRLALGCSESGETVSPFPAVNAWGSWKNFKTCYSTESQNSD- 593
Db 595 QSKDESEPKNALGVSEEMIVVSKQSSYNTLSGYEADGRNSWDSPFKHLVSEEQSLSEF 654
QY 594 ---QIKLLVTVEDTGVIPVDAQGRIFTPFMQADSSSTRTYGGTGIGLSISKRLVELMQ 649
Db 655 DISSNVRLMVSIEDTGIGIPLVAQGRVFMFPMQADSSSTRNYGGTGIGLSISKCLVELMR 714
QY 650 GEMGFVSEPGIGSTFSTGVFGKAETNTSITKLER--FDLAIQFTGLRALVIDNRNIRA 707
Db 715 GQINFISRPHIGSTFWFTAVLEKCDKCSAINHEMKPNVEHLPSTFKGKAIVVDKPVRA 774
QY 708 EVTRYELRRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKDAW----NK 753
Db 775 AVTRYHMKRLGINVDVVTSLKTAVVAAAFAERNGSPLPKPKQLDMILVEKDSWISTEDND 834
QY 754 EEFVSLDELFTRSKVTFTRVPKIFILLATSATLTERSEMKSTGLIDEVVIKPLRMSVLICC 813
Db 835 SEIRLLNSR-TNGNV-HHKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGAC 892
QY 814 LQETLVNGKKRQPNRQRN---LGHLLREKQILVDDNLVNRNRVAEGALKKYGAIVTCVE 870

Db 893 LQQVLELRKTRQOHPBGSSPATLKSLLTGKILVVDDNIVNRRVAAGALKKFGAEVVCAC 952
QY 871 SGKAALAMLKPPHNFDACFMDLQMPMDGFEATRRVRELEREINKKIASGEVSAEMFCKF 930
Db 953 SGQVALGLLQIPHFTFDACFMDIQMPQMDGFEATRQIRMMEKETKKTN-----1000
QY 931 SSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEFEVLYTAVARFFEP 980
Db 1001 LEWHLPIAMTADVIHATYEECLKSGMDGYVSKPFEENLYKSAKSEKP 1050

RESULT 15
AAE333694
ID AAE333694 standard; Protein; 1057 AA.
XX
AC AAE333694;
XX
DT 16-APR-2003 (first entry)
XX

Arabidopsis thaliana histidine kinase 4 (AHK4)-WOL, CRE1 protein.
Shoot formation; senescence; transgenic; transgenic plant; agriculture;
cell proliferation; shoot meristem formation; leaf development; AHK;
photosynthesis; histidine kinase; enzyme; CRE1.

Chimeric - Arabidopsis thaliana.
Chimeric - Unidentified.

WO200299079-A2.

12-DEC-2002.

06-JUN-2002; 2002WO-US18066.

06-JUN-2001; 2001US-296554P.

(GEHO) GEN HOSPITAL CORP.

Sheen J, Hwang I;

WPI; 2003-140613/13.

Increasing yield in plant, increasing shoot formation in a plant, or
delaying senescence in a plant such as wheat, rice, maize, barley,
potato, by using transgenes that regulate cytokinin response

Disclosure; Page 80-82; 87pp; English.

The present invention relates to a novel method of increasing yield in a
plant, increasing shoot formation or delaying senescence in a plant. The
method involves introducing into plant cells, a transgene having a B-type
response regulator operably linked to a promoter functional in plant
cells to yield transformed plant cells or whose expression reduces the
expression of A-type response regulator in the cells of the plant and
regenerating a plant from the transformed cells. The method is useful
for increasing the yield in a plant, increasing the shoot formation or
delaying senescence in a plant such as wheat, rice, maize, barley,
potato, tomato, soybean, tomato, oat, cotton and sunflower. The method
is useful for variety of agricultural and commercial purposes including
improving and enhancing photosynthesis, promoting cell proliferation,
shoot meristem formation, promoting leaf development, increasing crop
yields, improving crop and ornamental quality and reducing agricultural
production costs. The present sequence is Arabidopsis thaliana histidine
kinase 4 (AHK4)-WOL, CRE1 protein. This sequence is used to illustrate
the method of the invention.

Sequence 1057 AA;

Query Match 50.6%; Score 2539.5; DB 24; Length 1057;
Best Local Similarity 53.2%; Pred. No. 8.4e-213;
Matches 537; Conservative 152; Mismatches 240; Indels 81; Gaps 17;

QY 4 GERKEKVLQE--ALAPKKQQQRAQTSSRGAGRWKRNILLGILGVSFVW-WFWDTNE 60

Db 89 GNKKGSTFIQEHRA LLPKAL-----ILWIIIVGFISSGIYQWMDANK 131

QY 61 EIIMKRRETLANMCDERARVLQDQFNVSILNVHVALSILVSTFHHGKIPSAIDQRTFEEYT 120

Db 132 ---IRREEVLVSMCDQRARMLQDQFSVNVHVALAILVSTFHHKNPNSAIDQETFAEYT 188

QY 121 ERTNFERPLTSGVAYALKVPHSERЕКFEKEHGWAIKKMETEDQTVVQDCVPENFDPAPIQ 180

Db 189 ARTAFERPLLSGVAYAEKVVNFEREMFERQHNWVIKTM-----DRGEPSPVR 235

QY 181 DEYAPVIFAQETVSHIVSVDMSGEEDRENILRARASGKGLTSPFKLLKSNHGLGVLTFF 240

Db 236 DEYAPVIFSQDSVSYLESLDMSGEEDRENILRARETGKAVLTSPFRLLETHHGLGVLTFF 295

QY 241 AVYDTSLPDAPTEEQORVEATIGYLGASYDMPISLVEKLLHQASKQTIADVVDYDTTNTSGL 300

Db 296 PVYKSSLPENPTVEERIAATAGYLGGAFDVESLVENLLGQLAGNQAIVVHVYDITNASDP 355

QY 301 IKMYGS--EIGDISEQHISSLDFGDPSPRNHEMHCRPFKHKLPIPWTAITPSILVLVITFLV 358

Db 356 LVMYGNQDEEADRSLSHESKLDFGDPFRKHKMICRYHQKAPIPLNVLTTPVLFFAIGFLV 415

QY 359 GYILYEAINRIATVEEDCQKRELKARAEAAADIAKSOPLATVSHEIRTPMNGVGLMGLKML 418

Db 416 GYILYGAAMHIVKVEDDFHEMQELKVRAEAADVAKSQFLATVSHEIRTPMNGILGMLAML 475

QY 419 MDTDLDAKQMDYAQTAHSGKDLTSLINEVLDOAKIESGRLELENVFPDMRFILDNVSSL 478

Db 476 LDTELSSTQRDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSL 535

QY 479 LSGKANKEGIELAVYVSSQVPDVVVGDPSPRFRQIITNLVGNISIKFTQERGHIFISVHLAD 538

Db 536 FSEESRNKSIELAVFVSDKVPEIVKGDGSRFRQIILNLVGNVSKFT-EKGHIFVKVHLAE 594

QY 539 EVK---EPL-TIEDAVLKQRLALGCSEGETVSGFPAPVNAWGSWKNEKTCYSTESQNSD- 593

Db 595 QSKDESEPKNALNGGVSEEMIVSVKQSSYNLTSGYEAADGRNSWDSFKHLVSEEQSLSEF 654

QY 594 ----QIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSTSRTYGGTGIGLSISKRLVELMQ 649

Db 655 DISSNVRLMVSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNYGGTGIGLSISKCLVELMR 714

QY 650 GEMGFVSEPGIGSTFSFTGVFGKAETNTSTKLER--FDLAIQFTGLRALVIDNRNIRA 707

Db 715 GQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPSTFKGMKAIWDAKPVRA 774

QY 708 EVTRYELRRLGISADIVSSLRMACTCCISKLEN-----LAMILIDKDAW-----NK 753

Db 775 AVTRYHMKRLGINVDVWVTSLKTA VAAAAAFERNGSP LPTKPQLDMILVEKDSWISTEDND 834

QY 754 EEFVLDDELFTRSKVTFTVRPKIFLLATSATLTERSEMKSSTGLIDEVVIKPLRMSVLICC 813

Db 835 SEIRLLNSR-TNGNV-HHKSPKALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGAC 892

QY 814 LQETLVNGKKQPNRQRN---LGHLLREKQTLVVDDNLVNRNRVAEGALKKYGAIVTCVE 870

Db 893 LQQVLELRKTRQOHPEGSSPATLKSLLTGKKILVDDNIVNRNRVAAGALKKFGAEVVC AE 952

QY 871 SGKAALAMLKPPHNFDA CFMDLQMPEDMGFEATRVRRELEREINKKIASGEVSAEMFCKF 930

Db 953 SGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKETKKTN----- 1000

QY 931 SSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEFEVLYTAVARFEEP 980

Db 1001 LEWHPILAMTADVIHATYEECLKSGMDGYVSKPFEFEENLYKSVAKSPKP 1050

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OM protein - protein search, using sw model

Run on: November 28, 2003, 14:02:30 ; Search time 27.7424 Seconds
(without alignments)
6681.678 Million cell updates/sec

Title: US-09-918-508-4_COPY_32_1036
Perfect score: 5159
Sequence: 1 GIEDKSGLLVGSVGDLETKT.....ABQLYREVSRFFNSPSTTES 1005

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	5159	100.0	1036	10	US-09-918-508-4 Sequence 4, Appli
2	5001	96.9	1092	14	US-10-135-322-18 Sequence 18, Appl
3	3389.5	65.7	1044	15	US-10-101-464A-956 Sequence 956, App
4	3385	65.6	1002	15	US-10-101-464A-957 Sequence 957, App
5	2806.5	54.4	1270	15	US-10-101-464A-979 Sequence 979, App
6	2685.5	52.1	1176	10	US-09-918-508-2 Sequence 2, Appli
7	2674	51.8	1173	14	US-10-135-322-19 Sequence 19, Appl
8	2585.5	50.1	997	15	US-10-101-464A-977 Sequence 977, App
9	2544.5	49.3	890	15	US-10-101-464A-958 Sequence 958, App
10	2481.5	48.1	1057	10	US-09-918-508-6 Sequence 6, Appli
11	2475.5	48.0	1057	14	US-10-135-322-5 Sequence 5, Appli
12	2475.5	48.0	1057	14	US-10-135-322-24 Sequence 24, Appl
13	2462	47.7	974	15	US-10-126-120-2 Sequence 2, Appli
14	1368.5	26.5	480	15	US-10-101-464A-978 Sequence 978, App
15	1041	20.2	482	15	US-10-101-464A-955 Sequence 955, App

16	975	18.9	412	15	US-10-101-464A-905	Sequence 905, App
17	937.5	18.2	426	15	US-10-101-464A-124	Sequence 124, App
18	867.5	16.8	274	14	US-10-135-322-8	Sequence 8, Appli
19	849.5	16.5	289	14	US-10-135-322-10	Sequence 10, Appl
20	651	12.6	1018	15	US-10-101-464A-909	Sequence 909, App
21	639.5	12.4	1081	10	US-09-424-951-4	Sequence 4, Appli
22	620	12.0	1447	15	US-10-156-761-8624	Sequence 8624, Ap
23	600	11.6	170	15	US-10-101-464A-116	Sequence 116, App
24	563	10.9	2150	14	US-10-135-322-17	Sequence 17, Appl
25	560	10.9	971	14	US-10-116-048-2	Sequence 2, Appli
26	560	10.9	2471	14	US-10-116-048-4	Sequence 4, Appli
27	557.5	10.8	1240	15	US-10-101-464A-976	Sequence 976, App
28	552	10.7	1829	15	US-10-156-761-10049	Sequence 10049, A
29	543	10.5	816	15	US-10-101-464A-827	Sequence 827, App
30	525.5	10.2	747	12	US-10-100-294A-27	Sequence 27, Appl
31	504	9.8	129	15	US-10-101-464A-828	Sequence 828, App
32	500	9.7	185	15	US-10-101-464A-822	Sequence 822, App
33	480.5	9.3	1383	15	US-10-156-761-13096	Sequence 13096, A
34	474.5	9.2	1220	10	US-09-801-368-332	Sequence 332, App
35	470.5	9.1	418	10	US-09-424-951-2	Sequence 2, Appli
36	462	9.0	123	14	US-10-135-322-12	Sequence 12, Appl
37	462	9.0	139	15	US-10-101-464A-820	Sequence 820, App
38	458.5	8.9	738	12	US-10-171-404A-36	Sequence 36, Appl
39	448	8.7	717	12	US-10-171-404A-38	Sequence 38, Appl
40	439.5	8.5	496	15	US-10-101-464A-906	Sequence 906, App
41	408.5	7.9	1373	12	US-10-032-585-7129	Sequence 7129, Ap
42	405	7.9	264	15	US-10-101-464A-959	Sequence 959, App
43	378.5	7.3	762	15	US-10-101-464A-114	Sequence 114, App
44	359	7.0	206	15	US-10-101-464A-120	Sequence 120, App
45	345.5	6.7	104	14	US-10-135-322-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-09-918-508-4
; Sequence 4, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-4

Query Match	100.0%;	Score 5159;	DB 10;	Length 1036;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 1005;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GIEDKSGLLVGSVGDLEKTKMTTLKKKNKMWFWNKISSSGLKIPSFYSYQFLGSVKFNKAW	60	
Db	32	GIEDKSGLLVGSVGDLEKTKMTTLKKKNKMWFWNKISSSGLKIPSFYSYQFLGSVKFNKAW	91	
QY	61	WRKLVVVVFWVLVSIWTFWYFSSQAMEKRRKETLASMCDERARMLQDFNVSMNHVQAM	120	
Db	92	WRKLVVVVFWVLVSIWTFWYFSSQAMEKRRKETLASMCDERARMLQDFNVSMNHVQAM	151	
QY	121	SILISTFHGKIPSAIDQRTTFSEYTDRTSPERPLTSGVAYAMRVLHSEEREFEERQOGWTI	180	
Db	152	SILISTFHGKIPSAIDQRTTFSEYTDRTSPERPLTSGVAYAMRVLHSEEREFEERQOGWTI	211	

181	QY	RKMYSL	EQNPVHKDDYDLEALEPSPVQEEYAPVIFAQD	TVSHVVS	LDMLSGKEDREN	VLR	240		
212	Db	RKMYSL	EQNPVHKDDYDLEALEPSPVQEEYAPVIFAQD	TVSHVVS	LDMLSGKEDREN	VLR	271		
241	QY	ARSSGK	GVLTAPFPLIKTNRLGVILTF	FAVYKRD	LP	SNATPKERIEATNGYLG	VFDIESL 300		
272	Db	ARSSGK	GVLTAPFPLIKTNRLGVILTF	FAVYKRD	LP	SNATPKERIEATNGYLG	VFDIESL 331		
301	QY	VENLLQ	QASKQTILNVYDITNHSQPI	SMYGTN	VSADGLER	VSPLIFGDLR	KHEMR 360		
332	Db	VENLLQ	QASKQTILNVYDITNHSQPI	SMYGTN	VSADGLER	VSPLIFGDLR	KHEMR 391		
361	QY	FKQKPP	WPVLSMVTSGILVIALLV	VAHIIHAT	VSRIHK	VEEDCDKMKQLK	KKAEADVAK 420		
392	Db	FKQKPP	WPVLSMVTSGILVIALLV	VAHIIHAT	VSRIHK	VEEDCDKMKQLK	KKAEADVAK 451		
421	QY	SQFLAT	VSHEIRTPMNGVLGMLHMLMD	TELDVT	QDQYVRT	AQASGKALV	SLINEVLDQAK 480		
452	Db	SQFLAT	VSHEIRTPMNGVLGMLHMLMD	TELDVT	QDQYVRT	AQASGKALV	SLINEVLDQAK 511		
481	QY	IESGKLE	EEVRFDLRGILDDVLSL	FSSKSQ	KGVELAVYIS	DRVPM	LIGDPGRFRQIL 540		
512	Db	IESGKLE	EEVRFDLRGILDDVLSL	FSSKSQ	KGVELAVYIS	DRVPM	LIGDPGRFRQIL 571		
541	QY	TNLMGNS	IKFTEKGHIFVTVHLVD	ELFESID	GETASSPE	STLSGLPVADR	QRSWENFKAF 600		
572	Db	TNLMGNS	IKFTEKGHIFVTVHLVD	ELFESID	GETASSPE	STLSGLPVADR	QRSWENFKAF 631		
601	QY	SSNGHRS	FEPSPPDINLIVS	VEDTGV	GIPVEAQ	SRIFTPF	PMQVGP	SISRTHGGTGIGLSI 660	
632	Db	SSNGHRS	FEPSPPDINLIVS	VEDTGV	GIPVEAQ	SRIFTPF	PMQVGP	SISRTHGGTGIGLSI 691	
661	QY	SKCLVGL	MKGEGFSS	TPKVGSTFT	TAVFS	NGMQPAERK	NNNQPI	PFSEFRGMKAVVVD 720	
692	Db	SKCLVGL	MKGEGFSS	TPKVGSTFT	TAVFS	NGMQPAERK	NNNQPI	PFSEFRGMKAVVVD 751	
721	QY	HRPARAK	VS	WYHFQRLGIR	VEVPRVEQ	ALHYLKIGTT	TVNM	LIEQETWNREADDFIKK 780	
752	Db	HRPARAK	VS	WYHFQRLGIR	VEVPRVEQ	ALHYLKIGTT	TVNM	LIEQETWNREADDFIKK 811	
781	QY	LQKDPL	FLSPKILLANS	VESSI	SEALCT	GIDPP	IVIVKPL	RASMLAATLQ	RGLGIGIRE 840
812	Db	LQKDPL	FLSPKILLANS	VESSI	SEALCT	GIDPP	IVIVKPL	RASMLAATLQ	RGLGIGIRE 871

RESULT 2

US-10-135-322-18
; Sequence 18, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30

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; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 1092
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-18

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Query Match	96.9%;	Score 5001;	DB 14;	Length 1092;
Best Local Similarity	96.8%;	Pred. No. 0;		
Matches 979;	Conservative	0;	Mismatches	0; Indels 32; Gaps 1;
QY	1	GIEDKSGLLVGSVDLEKTKMTTLKKNKMFWFNKISSGLKIPSPSYQFLGSKVFNKAW	60	
Db	32	GIEDKSGLLVGSVDLEKTKMTTLKKNKMFWFNKISSGLKIPSPSYQFLGSKVFNKAW	91	
QY	61	WRKLVVVVWFVWLVSITWFVFPSSQAMEKRKETLASMCDERARMLQDQFNVMNHVQAM	120	
Db	92	WRKLVVVVWFVWLVSITWFVFPSSQAMEKRKETLASMCDERARMLQDQFNVMNHVQAM	151	
QY	121	SILISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREFEERQQGWTI	180	
Db	152	SILISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREFEERQQGWTI	211	
QY	181	RKMYSLEQNVPVHKDDYDLEALEPSPVQEEYAPVIFAQDTSVSHVSLDMLSGKEDRENVL	240	
Db	212	RKMYSLEQNVPVHKDDYDLEALEPSPVQEEYAPVIFAQDTSVSHVSLDMLSGKEDRENVL	271	
QY	241	ARSSGKGVLTAPFPLIKTNRLGVILTFVAVYKRDLPNSNATPKERIEATNGYLGVDIESL	300	
Db	272	ARSSGKGVLTAPFPLIKTNRLGVILTFVAVYKRDLPNSNATPKERIEATNGYLGVDIESL	331	
QY	301	VENLLQOLASKOTILNVVDITNHSQIPISMYGTNVSADGLERVSPLIFGDPLRKHEMR --	358	
Db	332	VENLLQOLASKOTILNVVDITNHSQIPISMYGTNVSADGLERVSPLIFGDPLRKHEMR	391	
QY	359	-----CRFKQKPPWPVLSMVTSGILVIALLV	388	
Db	392	YLQLAHTYVCNFFLFARIQVLTFCCELLPLCRFKQKPPWPVLSMVTSGILVIALLV	451	
QY	389	IHATVSRIHKVEEDCDKMKQKKAEADVAKSQFLATVSHEIRTPMNGVLGMLHMLMDT	448	
Db	452	IHATVSRIHKVEEDCDKMKQKKAEADVAKSQFLATVSHEIRTPMNGVLGMLHMLMDT	511	
QY	449	ELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLEEEVRFDLRGILDVLSLFS	508	
Db	512	ELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLEEEVRFDLRGILDVLSLFS	571	
QY	509	KSQKQGVELAVYISDRVPDMLIGDPGRFRQILTNLMGNSIKFTEKGHIFVTVHLVDLFE	568	
Db	572	KSQKQGVELAVYISDRVPDMLIGDPGRFRQILTNLMGNSIKFTEKGHIFVTVHLVDLFE	631	
QY	569	SIDGETASSPESTLSGLPVADRQSRWENKFAFSSNGHRSFEPSPDINLIVSVEDTGVGI	628	
Db	632	SIDGETASSPESTLSGLPVADRQSRWENKFAFSSNGHRSFEPSPDINLIVSVEDTGVGI	691	
QY	629	PVEAQSRIFTFPMQVGPISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTFTA	688	
Db	692	PVEAQSRIFTFPMQVGPISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTFTA	751	
QY	689	VFSNGMQPAERKNDNNQPIFSEFRGMKAVVDHRPARAKVSWYHFQRLGIRVEVPRVEQ	748	
Db	752	VFSNGMQPAERKNDNNQPIFSEFRGMKAVVDHRPARAKVSWYHFQRLGIRVEVPRVEQ	811	
QY	749	ALHYLKIGTTTTVMILIEQIWNREADDFIKKLQKDPFLSPKLIILLANSVSESSISEALC	808	
Db	812	ALHYLKIGTTTTVMILIEQIWNREADDFIKKLQKDPFLSPKLIILLANSVSESSISEALC	871	
QY	809	TGIDPPVIVKPLRASMLAATLQRLGIGIREPPQHKGPALILRNLLGRKILIVDDNN	868	
Db	872	TGIDPPVIVKPLRASMLAATLQRLGIGIREPPQHKGPALILRNLLGRKILIVDDNN	931	

QY	869	VNLRVAAGALKKYGADVCAESG	KAI	SAISLLKPPHEFDACFMDIQMP	MDGF	FEATRIRDM	928
Db	932	VNLRVAAGALKKYGADVCAESG	KAI	SAISLLKPPHEFDACFMDIQMP	MDGF	FEATRIRDM	991
QY	929	EEEMNKRIKNGEALIVENG	NKTSWHL	PVLAMTADVIQATHEE	CLKCGMDGY	979	
Db	992	EEEMNKRIKNGEALIVENG	NKTSWHL	PVLAMTADVIQATHEE	CLKCGMDGY	1042	

RESULT 3

US-10-101-464A-956

; Sequence 956, Application US/10101464A

; Publication No. US20030046728A1

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Nicolaas

; APPLICANT: Higgins, Colleen M.

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

; FILE REFERENCE: 11000.1020c2

; CURRENT APPLICATION NUMBER: US/10/101,464A

; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: 09/704,302

; PRIOR FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: 09/228,986

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/162,866

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: PCT/US00/00724

; PRIOR FILING DATE: 2000-01-11

; NUMBER OF SEQ ID NOS: 989

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 956

; LENGTH: 1044

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

US-10-101-464A-956

	Query Match	65.7%;	Score 3389.5;	DB 15;	Length 1044;
	Best Local Similarity	68.7%;	Pred. No. 3.5e-297;		
	Matches 686;	Conservative 97;	Mismatches 194;	Indels 21;	Gaps 7;
QY	17	EKTKMTTLKKKNM---	WFWNKISSGLKI-PSFSYQFLGSKFNKAWWRKLVVVVVVFV	72	
Db	38	EMTKAGFLGDGKMSLNL-	EKVLGVNYKIHPSHNSQAGSKFKRTWVRKVLWTWIIIG	96	
QY	73	VLVSIWTFWYFSSQAMEKKEBTLASMCDERARMLQDFNVSMNHVQAMSILISTFHHGKI	132		
Db	97	FIISACIFWYMSSQAAEKRETLGSMCDERARMLQDFNVSMNHVQAMSILISTFHHGKQ	156		
QY	133	PSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEREEREOQGWTIRKMYSLEQNPHV	192		
Db	157	PSAIDQTTTFERYTERTAFERPLTSFIAYAVRVLHCDREEFKAQGWIKRMDTVEKTPVH	216		
QY	193	KDDYDLEALEPSPVQEEYAPVIFAQDTSVHVSLDMLSGKEDRENVLRARSSGKGVLTAP	252		
Db	217	KDNSELESESPVQEEYAPVIFAQDTIGHVVSLDMLSGKEDRENVLRARASGKGVLTAP	276		
QY	253	FPLIKTNRLGVILTFVAVYKRDLPSPNATPKERIEATNGYLGGVFDIESLVENLLQOLASKQ	312		
Db	277	FRLIKTNSLGVILTFVAVYKNDLPNATPDERIEATDGYLGGAFFHIESLVEKLLQOLASKQ	336		
QY	313	TILVNVYDITNHSQIPISMYGTNVSADGLERVSPLIFGDPLEKHEMRCRFKQKPPWPVLSM	372		
Db	337	NIVNVYDTSNWSHPISMYGSDVSEDYLEHVSTLNFGDPFRKHEMRCRFKQKSPWPWLAI	396		
QY	373	VTSGILVIALLVAHIIHATVSRIRHKVEEDCDKMQLKKKAAADVAKSQFLATVSHEIR	432		
Db	397	TTSGILVIALLVGYIFQATVNRIAKVEDDYHKMVELKKRAEADVAKSQFLATVSHEIR	456		
QY	433	TPMNGVGLMHLMDTELDVTQDDYVRTAQASGKALVSLINEVLDAQIESGKLEEEVR	492		

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457 457 TPMNGVLGMLHMLMDTDLDETQDDYVRTAQESGKALVSLINEVLDAQIESGKIEIAVQ 516
QY 493 FDLRGILDDVLSLFSKQKGVELAVYISDRVPDMLIGDPGRFRQIILNLMGNSIKPTE 552
DB 517 FDLRAILDDVLSLFSGKQEKRVELAVYISENVPEKLIQDPGRFRQIILNLMGNSIKPTE 576
QY 553 KGHIFVTVHLVDLFEIDGETASSPESTLSGLPVADRQRSWENKFAFSNGHRSFEPS - 611
DB 577 KGHILVTVHLVDVMNSTDAEMESATRSLSGFPVPDRRLSWAKFRTESQGPASPVPSS 636
QY 612 -PPDINLIVSVEDTGVGIPVEAQSRIFTFPMQVGPISIRTHGGTGIGLSISKCLVGLMKG 670
DB 637 FSNPINLIISVEDTGIGIPPEAQPRVTFRFMQVGPISIRTHGGTGIGLSISKCLVGLMNG 696
QY 671 EIGFSSTPKVCSTFTTAVFSNGM-----QPAERKNDNNQPIFSEFRGMKAVVVDHR 722
DB 697 EIGFVSIPOVCGSTFTTAVFDDACSTSCKEKGQVKGQDGSQT---SEFHGMKALVVDTR 753
QY 723 PARAKVSWYHFQRLGIRVEVVPVVEQALHYLKIGITTTVMILIEQEIWNREAD--DFIK 779
DB 754 PVRANVSKYHIQRLGIHVEVADLNQCLHTIQSGNCRIDMWLLEWIDKDSGLSAIFLD 813
QY 780 KLQKDPLFLSPKLILLANSVESSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIR 839
DB 814 KLQDMKPRVSPRLFLLSNSISSSRMSGATTATGTPFVIMKPLRASMLVASFORVMGVNR 873
QY 840 EPPQHKGPALILRNLLGRKILIVDDNNVNLVAAAGALKKYGADVVAESGIKAISLLK 899
DB 874 ISCSNGESPSLFLRNLLRGRKILVDDNKVNLVAAEGALKKYGADVVDTSGEKAIALLR 933
QY 900 PPHEFDACFMDIQPMDGFPEATRRIRDMBEEMNKRIKNGEALIVENGKNTSWHLPLVAM 959
DB 934 PPHDFDACFMDIQPMDMGFEATKRIRQMEQTPSKEFLPGQSSSEPRENISNFHLPILAM 993
QY 960 TADVIQATHEECLKCGMDGYVSKPFEEQLYREVSRFFF 997
DB 994 TADVIHATHECTKYGMDGYVSKPFEEQLYREVSRFFF 1031

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RESULT 4
US-10-101-464A-957
; Sequence 957, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 1002
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-957

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Query Match	65.6%;	Score 3385;	DB 15;	Length 1002;
Best Local Similarity	68.1%;	Pred. No. 8.3e-297;		
Matches 685;	Conservative 115;	Mismatches 182;	Indels 24;	Gaps 6;
Qy	2	IEDKSGLLVGSVDLEKTKMTTLKKKNKMFWFNKISSSGLKIPSSYOFGLGSVKFNKAWW	61	

Db 1 MDAKTGLGDD-----GKISLNWRDKVLGKIVKIQHQYDHLFGSKKISNALW 47

QY 62 RKLVVVVVFWVLVSIWTFWYFSSQAMEKRKETLASMCDERARMLOQDFNVSMNHVQAMS 121

Db 48 RKLlyTWVFCATMFSLWIFSMSQAIEKRKETLASMCDERAQMLOQDFNVSMNHVQAMS 107

QY 122 ILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREEFERQOGWTIR 181

Db 108 ILISTFHHGKSPSAIDQRTFAEYTKRTAFERPLTSGVAYAVRVLHSERAEFKQOGWPIQ 167

QY 182 KMYSLEQNPNVHKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVLRA 241

Db 168 RMDTLEQNLVHKDDDFDPEVLEPSPIQEEYAPVIFAQDTVSHVVSIDLLSGKEDRENVLRA 227

QY 242 RSSGKGVLTAPEPLIKTNRLGVILTFVAVYKRDLPSPNATPKERIEATNGYLGGVFDIESLV 301

Db 228 RASGKGVLTAPEPLIKTNRLGVILTFVAVYKTDLPSPNATPDERIQATAGYIGGIFHIQSLV 287

QY 302 ENLLQQLASKQTIILVNVYDITNHSQPISMYGTNVVSADGLERSVPLIFGDPPLRKHEMRCRF 361

Db 288 EKLLQQLASKQNVLNVLDTTNQSHPISMYGSDEADDALEYVSTLNFEGDPFRKHEMRCRF 347

QY 362 KQKPPWPVLSMVTSGILVIALVAHIIHATVSRIHKVEEDCDKMQLKKKAEAAADVAKS 421

Db 348 KQKPPWPWLAIITSYGFLVIAMLTGHCYATVNRIAKVEDDYQKMMELKKQAEAAIAKS 407

QY 422 QFLATVSHEIRTPMNGVLGMLHMLMDTDLDTQDDYVRTAQASGKALVSLINEVLDQAKI 481

Db 408 QFLATVSHEIRTPMNGVLGMLHMLMDTDLDTQDDYVRTAQASGKALVSLINEVLDQAKI 467

QY 482 ESGKLELEEVVRDLRGILDVLSLFSSKSKQKGVELAVYISDRVPDMLIGDPGRFRQILT 541

Db 468 ESGKLELEAVQFDLRAILDVLSLFSGSKQKGVELAVFISDQVPEKLIIGDPGRFRQIIT 527

QY 542 NLMGNSIKFTEKGHIFVTVHLVDELFEISIDGETASSPESTLSGLPVPADRQRSWENFKAFS 601

Db 528 NLMGNSIKFTEKGHIFVTVHLAQEVMDSLDVETESSKNTLSGFQVABERRLSWAKFKTFS 587

QY 602 SNGH-RSFEPSPD- INLIVSVEDTGVGIPVEAQSRIFTPFMQVGPSISRTHGGTGIGLS 659

Db 588 QHERVCSYSPSTDVLINLIVSVEDTGVGIPPEAQRVFTPFMQVGPSISRTHGGTGIGLS 647

QY 660 ISKCLVGLMKGEICFSPSTPKVGSTFTTFAVNSGMQ-----PAERKNDNNQPIFSEFRGM 714

Db 648 ISKCLVELMNGEVGFSIPNVGSTFTTFAVFNNGHSLNLEYTCQQMNNQSNANSSEFEGM 707

QY 715 KAVVVDHRPARAKVSWYHFQRLGIRVEVVPVEQALHYLKIGITTTVNMILLIEQEIWNREA 774

Db 708 SALVVDPRSVRAKVSKYHVQRLGIOVEIVSDLNQVLSLKSRRKPRIDMVLIIEEVWNDS 767

QY 775 D---DFIKKLQKDPLFLSPKILLANSVSESSISEALCTGIDPPIVIVKPLRASMLAATLQ 831

Db 768 DLSILFVDQLRHIDQKVTPrLFLLAKSISSTRSDNVTCDTHSPAVIMKPLRASMVAACLQ 827

QY 832 RGLG-IGIREPPQHKGPPALILRNLLGRKILTVDDNNVNLRVAAGALKKYGADVCAES 890

Db 828 RTWGNMGNKGNRYNGEVSRLSLQHLLLGRKILTVDDNKVNLKVAAGALKRYGAELVCVES 887

QY 891 GIKAISLLKPPHEFDACFMDIQMPEDMGFEATRIRIRDMEEEMNKRIKNGEALIVENGKNT 950

Db 888 GKEAISLLTPPHSFYACFMDIQMPGMDGFEATKIRDVESVNRKIQLGEVSAEAHGVL 947

QY 951 SWHLPVLAMTADVIQATHEECLKCGMDGYVSKPFEABQLYREVS RF 996

Db 948 NWHVPILAMTADVIHATQEECMKCGMDGYVSKPFEABQLYREVS RF 993

RESULT 5
US-10-101-464A-979
; Sequence 979, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 979
; LENGTH: 1270
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-979

Query Match 54.4%; Score 2806.5; DB 15; Length 1270;
Best Local Similarity 58.8%; Pred. No. 3e-244;
Matches 570; Conservative 148; Mismatches 212; Indels 39; Gaps 11;

QY 60 WWRKLVVVVFWVLVSIWTFWYFSSQAMEKRKETLASMCDERARMLOQDFNVSMNHVQA 119

Db 311 WRKLLIVFVWAGVMTSIWLFHLYAKNVLRRREETLANMCDERARMLOQDFNVSMNHVA 370

QY 120 MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREEFERQOGWT 179

Db 371 LAILVSTFHHGKQPSAIDQKTFFEYTERTAERPLTSGVAVALKVPHSEREQFEKRHDWT 430

QY 180 IRKMSYLEQNPNVHKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVL 239

Db 431 IKKMETADQTLV--PDYMLDRLDPAPIQDEYAPVVFSSQETVSHIVSIDMMSGKEDRENIL 488

QY 240 RARSSGKGVLTAPEPLIKTNRLGVILTFVAVYKRDLPSPNATPKERIEATNGYLGGVFDIES 299

Db 489 RARASGKGVLTSPPFKLLKSNHLGVVLTFAVYDRELPAATAEQRIEATVGYLGASYDVPS 548

QY 300 LVENLLQQLASKQTIILVNVYDITNHSQPISMYGTNVVSADGLERSVPLIFGDPPLRKHEMRC 359

Db 549 LVEKLLHQLASKQTIIVNVYDITNGSAPINMYGDDVIDTGLVRVSNVDVFGDPLRRHEMHC 608

QY 360 RFKQKPPWPVLSMVTSGILVIALVAHIIHATVSRIHKVEEDCDKMQLKKKAEAAADVA 419

Db 609 RFKQRPPLPWTAINSSVGLLVITLLVGHIFHAAINRIAKVEEDYRQMMEKLSRAEAAADVA 668

QY 420 KSQFLATVSHEIRTPMNGVLGMLHMLMDTDLDTQDDYVRTAQASGKALVSLINEVLDQA 479

Db 669 KSQFLATVSHEIRTPMNGVLAMQLMDTNLNNANQLDYAQTAHACGKDLISLINEVLDQA 728

QY 480 KIESGKLELEEVVRDLRGILDVLSLFSSKSKQKGVELAVYISDRVPDMLIGDPGRFRQI 539

Db 729 KIESGKLELEKVPFDLRLALDNLVSLISGRSNEKGIELAVYISDRVPEAVIGDPGRFRQI 788

QY 540 LTNLMGNSIKFTEKGHIFVTVHLVDE-----LFESIDGETASSPESTLSGLP 586

Db 789 ITNLVGNISIKFTEGHIFVSVHLLLEGCSQHDFRDVEKRLSSNLVEDTSDKTFNTLSGFQ 848

QY 587 VADRORSWENFKAFSSNGHRSFPPDPDINLIVSVEDTGVGIPVEAQSRIFTPFMQVGRS 646

Db 849 VVDRRKSWEFRKKNLNRSDQIDVNES---VEVLVTVEDTGVGIAREAQSRIFTTFFVQADSS 905

QY 647 ISRTHGGTGIGLSISKCLVGLMKGEIGFSSSTPKVGSTFTTFAVFSN-GMQPAERKNDNNQ 705

Db 906 TSRTYGGTGIGLSISKCLVDLMHGEIGFVSEPGTGSTTFTVPPFAKCEMNCLEVKGQNYD 965

QY 706 PIFSEFRGMKAVVVDHRPARAKVSWYHFQRLGIRVEVVPVEQALHYLKIGT-----TTV 760

Db 966 SIISEFRGLRALVIDKXHIRAEVARYHLERLRISVDVACSLKSACTYLSNSSSPRELSDF 1025
QY 761 NMILIEQEIWNREAD-----DFIKKLQ--KDPFLFSLPKLILLANSVSESSISEA--LCTG 810
Db 1026 DMVLIDKDVWDROTGLELNSLWKHRQNGSGVSRPKIFLLATSI-SPIEHSCLKLANL 1084
QY 811 IDPPIVIVKPLRASMLAATLQRLGIGIREPPQHKGPPALILRNLLGRKLIVDDNNVN 870
Db 1085 VDN--VLAKPLRLSVLISFLQELGNGKKRLSDRR--KVSTLGSLLKGRRLVYDDNLVN 1140
QY 871 LRVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMPMDGFATRRIRDMEE 930
Db 1141 RRVAEGALKKYGAIVTCVSGKDAVAKLQPPHDFACFMDLQMPMDGFATRRIRHLES 1200
QY 931 EMNKRIKNGEALIVENGKNTSWHLPLVLTADVIOATHEECLKCGMDGYVSKPPEAEQLY 990
Db 1201 EVNSKIASGEVSSDAFQNVVHHTPILTADVIOATNEECLKCGMDGYVSKPPEEQLY 1260
QY 991 REVSRRFNS 999
Db 1261 SAVARFFES 1269

RESULT 6
US-09-918-508-2
; Sequence 2, Application US/09918508
; Patent No. US20020177162A1
; GENERAL INFORMATION:
; APPLICANT: KAKIMOTO, TATSUO
; APPLICANT: HIGUCHI, MASAYUKI
; APPLICANT: INOUE, TSUTOMU
; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY
; TITLE OF INVENTION: TO CYTOKININ RECEPTOR
; FILE REFERENCE: Q65478
; CURRENT APPLICATION NUMBER: US/09/918,508
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: JP 2001-073812
; PRIOR FILING DATE: 2001-03-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1176
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-918-508-2

Query Match 52.1%; Score 2685.5; DB 10; Length 1176;
Best Local Similarity 57.2%; Pred. No. 2.4e-233;
Matches 551; Conservative 142; Mismatches 224; Indels 47; Gaps 13;
QY 61 WRK-LVVVVVFWVLVSIWTFWYFSSQAMEKREKTELASCMCDERARMLQDQNVSMNHVQA 119
Db 230 WRKNILLGIILGGVSFVWFWDTNEEIIKRRRETLANMCDERARVLQDQNVSLNHVHA 289
QY 120 MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEFEFERQQGWT 179
Db 290 LSILVSTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYALKVPHSREKFEKEHGW 349
QY 180 IRKMYSLQNPVHKDDYDLEALEPSPVQEEYAPVIPAQDTVSHVSLDMLSGKEDRENVL 239
Db 350 IKKMETEDQTVV--QDCVPENFDPAPIQDEYAPVIPAQETVSHIVSDMMSGEEDRENIL 407
QY 240 RARSSGKGLTAPFPLIKTNRLGVLITFAVYKRDLPNSNATPKERIEATNGVLGGVFDIES 299
Db 408 RARASGKGLTSPFKLLKSNHLGVLITFAVYDTSILPPDATEEQRVEATIGLGASYDMPS 467
QY 300 LVENLLQQLASKQTLVNVVYDITNHSQPISMYGTNVNSADGLERVSPLIFGDLRKHEMRC 359
Db 468 LVEKLLHQLASKQTLIAVDVYDTTNTSGLIKMYGSEIGDISEQHISSLDLDFGDSRNHEMHC 527
QY 360 RFKQKPPWPVLSMTVTSFGILVIALLVAHIIHATVSRHKEVEDCDKMKQLKKAAEADVA 419

Db 528 RFKHKLPWPWTAITPSILVLVITFLVGYILYEAIRNRIATVEEDCQKMKRELKARAEADIA 587
QY 420 KSQFLATVSHEIRTPMNGVGLMLHMLMDTDLDTQDDYVRTAQASGKALVSLINEVLDOA 479
Db 588 KSQFLATVSHEIRTPMNGVGLMLKMLMDTDLDAKQMDYAQTAGSGKDLTSLINEVLDOA 647
QY 480 KIESGKLELEEVRFDLRGILDVLSLFSSKSOQKGVELAVYISDRVPDMLIGDPGRFRQI 539
Db 648 KIESGRLELENVFPDMRFILDVNVSSLLSGKANEGIELAVYSSQVDPVVVDPSRFRQI 707
QY 540 LTNLMGNSIKFT-EKGHIFVTVHLVDELPEESIDGETA-----SSPESTLSGLPVA 588
Db 708 ITNLVGNISIKFTQERGHIFISVHLADEVKEBELTIEDAVLKQRLALGCSSESGETVSGFP 767
QY 589 DRQSWENFK-AFSSNGHRSFEPSPDINLIVSVEDTGVGIPVEAQSRIFTTFPMQVGPSI 647
Db 768 NAWGSWKNFKTCYSTESQNS-----DQIKLLVTVEDTGVGIPVDAQGRIFTTFPMQADSST 822
QY 648 SRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSSTFTTAVFSNGMQPAERKNDNNQPI 707
Db 823 SRTYGGTGIGLSISKRLVELMQEMGFVSEPGIGSTFSFTGVFG-----KAETNTSI 874
QY 708 -----FSEFRGMKAVVVDHRPARAKVSWYHFORLGRVVEVPRVEQALHYLKIGTT 758
Db 875 TKLERFDLAIQEFGLRALVIDNRNIRAEVTRYELRRLGISADIVSSLRMACTCCISKLE 934
QY 759 TVNMILIEQEIWNREADDFIKKL--QKDPFLFSLPKLILLANSVE-SSISEALCTG-IDP 813
Db 935 NLAMILIDKDAWNKEEFSVLDELFTRSKVTFTRVPKIFLLATSATLTERSEMKTGLIDE 994
QY 814 PIVIVKPLRASMLAATLQRLGIGIREPPQHKGPPALILRNLLGRKLIVDDNNVNLRV 873
Db 995 --VVIKPLRMSVLI CCLQETLVNGKKRQPNRQ---RRNLGHLRLREKQILVVDNVLNRRV 1049
QY 874 AAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMPMDGFATRRIRDMEEEMN 933
Db 1050 AEGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMPMDGFATRRVRELEREIN 1109
QY 934 KRIKNGEALIVENGKNTSWHLPLVLTADVIOATHEECLKCGMDGYVSKPPEAEQLYREV 993
Db 1110 KKIASGEVSAEMFCKFSSWHVPILMTADVIOATHEECLKCGMDGYVSKPPEEVLVTAV 1169
QY 994 SRFF 997
Db 1170 ARFF 1173

RESULT 7
US-10-135-322-19
; Sequence 19, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1173
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-19

Query Match 51.8%; Score 2674; DB 14; Length 1173;

Best Local Similarity 57.0%; Pred. No. 2.6e-232;		Matches 549; Conservative 142; Mismatches 224; Indels 48; Gaps 13;	
Qy	61	WRK-LVVVWVFWVLVSIWTFWFYFSSQAMEKRKKTASMCDERARMLQDQFNVSMNHVQA	119
Db	230	WRKNILLGILGGVSFVWFWDTNEEIMKRRETLANMCDERARVLQDQFNVSLNHVHA	289
Qy	120	MSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREFERQQGWT	179
Db	290	LSILVSTFHHGKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSEREKFEKEHGWA	349
Qy	180	IRKMYSLQNPVHKDDYDLEALEPSVQBEYAPVIFAQDVTSHVVSILDMLSGKEDRENVL	239
Db	350	IKKMETEDQTVV--QDCVPENFDPAPIQDEYAPVIFAQETVSHIVSDVMMSGEEDRENIL	407
Qy	240	RARSSGKGLTAPFPLIKTNRLGVILTFVYVKRDLPSNATPKERIEATNGYLGVFVDES	299
Db	408	RARASGKGLTSPFKLLKSNHLGVVLTFVYDTSLPDPDATEEQRVEATIGYLGASYDMP	467
Qy	300	LVENLLQOLASKQTLILNVYDITNHSQIPSMYGTNVVSADGLERVSPLIFGDPPLRKHEMRC	359
Db	468	LVEKLLHQASKQTLIADVDDYDTTNTSGLIKMYGSEIGDISQHISSLDGDPDSRNHEMHC	527
Qy	360	RFKQKPPVPLSMVTSFGILVIALVAHIHATVSRHKVEEDCDKMKLKKKAEAADVA	419
Db	528	RFKHKLPWPATPISILVLVITFLVGYILYEAINRIATVEEDCQKRELKARAEAAADIA	587
Qy	420	KSQFLATVSHERTPMNGVLGMLHMLMDTDLVDTQDYYRTAQASGKALVSLINEVLDOA	479
Db	588	KSQFLATVSHERTPMNGVLGMLKMLMDTDLDAKQMDYAQTAGSGKDLTSLINEVLDOA	647
Qy	480	KIESGKLELEEVRFDLRGILDVLSLFSSKSQQKGVELAVYISDRVPMILIGDPGRFRQI	539
Db	648	KIESGRLELNVFPDMRFILDNVSSLLSGKANEGIELAVYSSQVDPVVVGDPSPRFRQI	707
Qy	540	LTNLMGNSIKFTEKGHIFVTVHLVDELFESIDGETA-----SSPESTLSGLPVAD	589
Db	708	ITNLVGNSTK--ERGHIFISVHLADEVKEPLTIEDAVLKQRLALGCSGESGTVSGFPVAVN	765
Qy	590	RQRSWENFK-AFSSNGHRSFEPSPPDINLIVSVEDTGVGIPVEAQSRIFTFPMQVGPSIS	648
Db	766	AWGSWKNFKTCYSTESONS-----DQIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSTS	820
Qy	649	RTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVSGSTFTTAVFSNGMQPAERKNDNNQPI-	707
Db	821	RTYGGTGIGLSISKRLVELMQGEMGFVSEPGIGSTFSFTGVFG-----KAETNTSIT	872
Qy	708	-----FSBFRGMKAVVDHRPARAKVSWYHFQRLGIRVEVVPRVQALHYLKIGTTT	759
Db	873	KLERFDLAIQFTGLRALVIDNRNIRAETRYELRRLGISADIVSSLRMACCTCCISKLEN	932
Qy	760	VNMILIEQEIWNREADDFIKKL--QKDFLFLSPKLILLANSVE-SSISEALCTG-IDPP	814
Db	933	LAMILIDKAWNKEEFSVLDLFTRSKVTFTRVPKIFLLATSATLTERSEMKTGLIDE-	991
Qy	815	IVIVKPLRASMLAATLQRLGIGIREPPQHKGPPALILRNLLGRKILIVDDNNVNLRVA	874
Db	992	-VVIKPLRMSVLICCLQETLVNGKKRQPNRQ---RRNLGHLRLREXQILVWDDNLVNRVA	1047
Qy	875	AGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMPMDGFEATRRIIDMEEMNK	934
Db	1048	EGALKKYGAIVTCVESGKAALAMLKPPHPNFDACFMDLQMPMDGFEATRVRVLEEREINK	1107
Qy	935	RIXNGEALIVENGKNTSWHLPLVAMTADVIQATHEECLKGMDGYVSKPFPEAEQLYREVS	994
Db	1108	KIASGEVSAEMFCKPSSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFPEEVLYTAVA	1167
Qy	995	RFF 997	
Db	1168	RFF 1170	

US-10-101-464A-977		; Sequence 977, Application US/10101464A	
		; Publication No. US20030046728A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Strabala, Timothy	
		; APPLICANT: Nieuwenhuizen, Nicolaas	
		; APPLICANT: Higgins, Colleen M.	
		; TITLE OF INVENTION: Compositions Isolated from Plant Cells	
		; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling	
		; FILE REFERENCE: 11000.1020C2	
		; CURRENT APPLICATION NUMBER: US/10/101,464A	
		; CURRENT FILING DATE: 2002-03-18	
		; PRIOR APPLICATION NUMBER: 09/704,302	
		; PRIOR FILING DATE: 2000-11-01	
		; PRIOR APPLICATION NUMBER: 09/228,986	
		; PRIOR FILING DATE: 1999-01-12	
		; PRIOR APPLICATION NUMBER: 60/162,866	
		; PRIOR FILING DATE: 1999-11-01	
		; PRIOR APPLICATION NUMBER: PCT/US00/00724	
		; PRIOR FILING DATE: 2000-01-11	
		; NUMBER OF SEQ ID NOS: 989	
		; SOFTWARE: FastSeq for Windows Version 4.0	
		; SEQ ID NO 977	
		; LENGTH: 997	
		; TYPE: PRT	
		; ORGANISM: Eucalyptus grandis	
		US-10-101-464A-977	

Query Match 50.1%; Score 2585.5; DB 15; Length 997;	
Best Local Similarity 53.8%; Pred. No. 2.1e-224;	
Matches 536; Conservative 160; Mismatches 228; Indels 73; Gaps 14;	

Qy	48	YQFLGSVKFNKAWMRKLVVWVFWVLVSIWTFWFYFSSQAMEKRKKTASMCDERARMLQ	107
Db	26	YTFIQS--NRAWIPKILVLSVVGMAFLSMSIYRKMADAIKVRKKEVLVSMCDQORARMLK	82
Qy	108	DQENVSMNHVQAMSILISTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHS	167
Db	83	DQFSVSNHVHALAILVSTFHYKNPSAIDQETFAEYRTARTAFERPLLSGVAYAEVRTNS	142
Qy	168	EREFEERQQGWTIRKMYSLQNPVHKDDYDLEALEPSVQBEYAPVIFAQDVTSHVVSILD	227
Db	143	EREKPEEQHGWTIKTMEX-----QPSVRDEYAPVIFSQETVSYIESLD	186
Qy	228	MLSCKEDRENVLRRSSGKGLTAPFPLIKTNRLGVILTFVYVKRDLPSNATPKERIEAT	287
Db	187	MMSGEEDRENILRRATGKAVLTSPFRLLGSHHLGVVLTFPPVYKSKLPPNPPTVEERIEAT	246
Qy	288	NGVLGVDFDIESLVENLLQOLASKQTLILNVYDITNHSQIPSMYGTNVSA--DGLERVSP	345
Db	247	VGYLGAFDVESLVENLLGQLDGNQAILNVYDVTNSBPPLIMYGHQYQECDSLHESK	306
Qy	346	LIFGDPPLRKHEMRCRFKQKPPVPLSMVTSFGILVIALVAHIHATVSRHKVEEDCDK	405
Db	307	LDFGDPFRKHQMICRYHQKAPPSWTALTTAFFVFVIGLLVGYILYGAATHIVKVEDDFHE	366
Qy	406	MKOLKKKAEAADVAKSQFLATVSHSHEIRTPMNGVLGMLHMLMDTELDTVQQDYVRTAQASG	465
Db	367	MQELKVRAEAADVAKSQFLATVSHSHEIRTPMNGILGMLALLDTELSSTQRDYAQTAICG	426
Qy	466	KALVSLINEVLDOAKIESGKLEEEVRFDLRGILDVLSLFSSKSQQKGVELAVYISDRV	525
Db	427	KALIALINEVLDRAKIEACKLELETVPFDIRSILODVLSLFSESRHKGIELAVFVADKV	486
Qy	526	PDMLIGDPGRFRQILTNLMGNSIKFTEKGHIFVTVHLVDELFESIDGETAS----SPE--	579
Db	487	PEIVMGDPGRFRQIITNLVGNVSKFTEKGHIFVKVHLADQVKGATNAHAKTCLNGRPEED	546
Qy	580	-----STLSGLPVADRQRSWENFKAF-----SSNGHRSFEPSPPDINLIVSVED	623
Db	547	ILISDGSQLETLSGCEVADERNSDWTFNLLVAEDQNVSVDNMTSNEASENVTVMVSVED	606
Qy	624	TGVGIPVEAQSRIFTFPMQVGPSISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGST	683

Db 607 TGIGIPLAQRVEMPFMQADSSSTRTYGGTIGLSTSKCLVELMGGHINFISRPQIGST 666

QY 684 FTFTAVFSNGMQPAERKNDNN-----QPIFSEFRGMKAVVVDHRPARAKVSWTHFQRLGI 738

Db 667 FSFTAVFGR-----CKRLVFANVKRTFEDLPSGFGKGLKAIIVDVGKPVRAAVTRYHLNRLGI 722

QY 739 RVEVVPRVEQAL-----HYLKIGTTTVNMILIEQEIWNREADDFIKKL-----QKDPLF 787

Db 723 NVEVASSINAITATGKGKNSLTAGYRHPDIIILVEKDMWMSSIDSWSISLTVADWKQNGNLI 782

QY 788 LSPKLIILLANSVESSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIGIREPPQ---- 843

Db 783 QLPKILLASKISASELERAKASGF-ADTVIMKPVRASMLAACLOQVLGIGRKKQLQKDMN 841

QY 844 -HKGPPALILRNLLGRKILIVDDNNVNLRVAAGALKKYGADVCAESGIKAISSLKPPH 902

Db 842 MRNGSSA--LRSLLYGKKILVVDDNKVNRRAAGALKKPGANVECAESGKAALLELLQLPH 899

QY 903 EFDACFMDIQPEMDGFEATRIRDMEEEMNKRIKNGEALIVENGKNTSWHLPLVAMTAD 962

Db 900 DFDACFMDIQPEMDGFEATRQIRLMESQVNEQMKSESQVAVQIVKGGE--WHMPILAMTAD 957

QY 963 VIQATHEECLKCGMDGYVSKPFEAEQLYREVSRFFNS 999

Db 958 VIHATYDECLKCGMDGYVSKPFPDEENLYQAVAKFFRT 994

RESULT 9

US-10-101-464A-958

; Sequence 958, Application US/10101464A

; Publication No. US20030046728A1

; GENERAL INFORMATION:

; APPLICANT: Strabala, Timothy

; APPLICANT: Nieuwenhuizen, Nicolaas

; APPLICANT: Higgins, Colleen M.

; TITLE OF INVENTION: Compositions Isolated from Plant Cells

; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

; FILE REFERENCE: 11000.1020c2

; CURRENT APPLICATION NUMBER: US/10/101,464A

; CURRENT FILING DATE: 2002-03-18

; PRIOR APPLICATION NUMBER: 09/704,302

; PRIOR FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: 09/228,986

; PRIOR FILING DATE: 1999-01-12

; PRIOR APPLICATION NUMBER: 60/162,866

; PRIOR FILING DATE: 1999-11-01

; PRIOR APPLICATION NUMBER: PCT/US00/00724

; PRIOR FILING DATE: 2000-01-11

; NUMBER OF SEQ ID NOS: 989

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 958

; LENGTH: 890

; TYPE: PRT

; ORGANISM: Eucalyptus grandis

US-10-101-464A-958

Query Match 49.3%; Score 2544.5; DB 15; Length 890;

Best Local Similarity 58.4%; Pred. No. 8.7e-221;

Matches 523; Conservative 133; Mismatches 201; Indels 39; Gaps 11;

QY 133 PSAIDQRTFSEYTDRTSPERPLTSGVAYAMRVLHSEEREEFERQQGWTIRKMYSLQNVPVH 192

Db 4 PSAIDQKTFGYEYTERTAFAERPLTSGVAYALKVPHSEREQFEKRHDWTIKMETADQTLV- 62

QY 193 KDDYDLEALEPSPQEEYAPVIFAQDITVSHVSLDMLSGKEDRENVLRARSSGKGVLTAP 252

Db 63 -PDYMLDRLDPAPIQDEYAPVVFSEQETVSHVSIIDMMSGKEDRENILRARASGKGVLTSP 121

QY 253 FPLIKTNRLGLVILTFAYVKRDLPSNATPKERIEATNGYLGGVFDIESLVENLLQQALASKQ 312

Db 122 FKLLKSNHLGVVLTFAVYDRELPADEQRIEATVGYLGASYDVPSLVKELLHLQALASKQ 181

QY 313 TILVNVYDITNHSQIPISMYGTNVNSADGLERVSPLIFGDLPLRKHEMCRFKQKPPWPVLSM 372

Db 182 TIVNVYDITNGSAPINMYGDDVIDTGLVRVSNVDFGDLRRHEMCHRCFKQPPPLPWTAI 241

QY 373 VTSFGILVIALIVAHIIHATVSRHKVEEDCDKWKQLKKKAAEADVAKSQFLATVSHEIR 432

Db 242 NSSVGLLVITLLVGHIFHAAINRIAKVEEDYRQMMELKSRAEADVAKSQFLATVSHEIR 301

QY 433 TPMNGVLGMLHMLMDTELDVTQDDYVRTAQASGKALVSLINEVLDQAKIESGKLEEEVR 492

Db 302 TPMNGVLAMLQMLMDTNLANQLDYAQTAHACGKDLISLINEVLDQAKIESGRLELEKVP 361

QY 493 FDLRGILDDVLSLFSKSKSQKGVELAVYISDRVDPMLIGDPGRFRQILTNLMGNSIKFTE 552

Db 362 FDLRLALDNVLSLISGRSNEKIELAVYVSDRVPFAVIGDPGRFRQIITNLVGNISIKFTH 421

QY 553 KGHIFVTVHLVDE-----LFESIDGETASSPESTLSGLPVDADRQRSWENFKA 599

Db 422 EGHIFVSVHLLHEGCSQHDFRDVEKRLSSNLVEDTSDKTFTNTLSGFQVVDRRKSWERFKK 481

QY 600 FSSNGHRSFEPSPDINLIVSVEDTGVGIVPEAQSRIFTFPMQVGPISRTHGGTGIGLS 659

Db 482 LNRSDQIDVNES---VEVLTVVEDTGVGLAREAQSRIFTFFVQADSTSTRTYGGTGIGLS 538

QY 660 ISKCLVGLMKGEIGFSSTPKVGSTFTTFAVFSN-GMQPAERKNDNNQPIFSEFRGMKAVV 718

Db 539 ISKCLVDLMHGEIGFVSEPGTGSTFTSFVFAKCEMNCLEVKGNQYDSIIFSEFRGLRALV 598

QY 719 VDRPARAKVSWYHFQRLGIRVEVVRVEQALHYLKIGT-----TTVMILIEQEIWNRE 773

Db 599 IDKRHIRAEVARYHLERLRISVDVACSLKSACTYLSNSSSPRELSDFDVLIDKDVWDRQ 658

QY 774 AD-----DFIKKLQ--KDPLFLSPKLILLANSVESSISEA---LCTGIDPPIVIVKPLRA 823

Db 659 TGLELNISLWKHRQNGSVSIRPKIFLLATSI-SPIEHSELKLANLVDN--VLAKPLRL 715

QY 824 SMLAATLQRLGIGIGIREPPQHKGPPALILRNLLGRKILIVDDNNVNLRVAAGALKKYGA 883

Db 716 SVLISFLQEAALGNKKRLSDRR--KVSTLGSLLKGRRLVDDNLVNRVAEGALKKYGA 773

QY 884 DVVCAESGIKAISLLKPPHEFDACFMDIQPEMDGFEATRIRDMEEEMNKRIKNGEALI 943

Db 774 IVTCVSGKDAVAKLQPPHDFAAACFMDLQPEMDGFEATRQIRHLESEVNSKIASGEVSS 833

QY 944 VENGKNTSWHLPLVAMTADVIQATHEECLKCGMDGYVSKPFEAEQLYREVSRFFNS 999

Db 834 DAFQNVVWHHTPILAMTADVIQATNEECLKCGMDGYVSKPFEAEQLYSAVARFFES 889

RESULT 10

US-09-918-508-6

; Sequence 6, Application US/09918508

; Patent No. US20020177162A1

; GENERAL INFORMATION:

; APPLICANT: KAKIMOTO, TATSUO

; APPLICANT: HIGUCHI, MASAYUKI

; APPLICANT: INOUE, TSUTOMU

; TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY AND ANTAGONIST-ACTIVITY

; TITLE OF INVENTION: TO CYTOKININ RECEPTOR

; FILE REFERENCE: Q65478

; CURRENT APPLICATION NUMBER: US/09/918,508

; CURRENT FILING DATE: 2001-08-01

; PRIOR APPLICATION NUMBER: JP 2001-073812

; PRIOR FILING DATE: 2001-03-15

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 1057

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-918-508-6

Query Match 48.1%; Score 2481.5; DB 10; Length 1057;

Best Local Similarity 50.9%; Pred. No. 5.9e-215; Matches 536; Conservative 156; Mismatches 250; Indels 111; Gaps 18;			
Qy	21	MTTLKKKNKMFWNKISSSGLKIPSPS-----YQFLGSVKFN-----	57
Db	43	LNSSEKPRKIDFWR----SGLM--GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTF	96
Qy	58	----KAWWRKLVVVVWVFWVLVSIWTFWYFSSQAMEKREKETLASMCDERARMLQDQFNVS	113
Db	97	IQEHRALLPKALILWIIIVGFISSGIYQWMDANKIRREEVLSVMSCDQARMLQDQFSVS	156
Qy	114	MNHVQAMSIISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEEFE	173
Db	157	VNHVHALAILVSTFHYHKNPSAIDQETFAEYTARTAFERPLLSGVAYAEKVNFEREMFE	216
Qy	174	RQCGWTIRKMYSLEQNPFVKDDYDLEALEPSPVQEEYAPVIFAQDTSVSHVSLDMLSGKE	233
Db	217	RQHNWVIKTM-----DRGEPSVRDEYAPVIFSQDSVSYLESLDMMSGEE	261
Qy	234	DRENVLRARSSGKGVLTAPPPLIKTNRLGVILTFVAVYKRDLPSPNATPKERIEATNGYLG	293
Db	262	DRENILRARETGKAVLTSPFRLLETHHLGVLTFFPVYKSSLPENPTVEERIAATAGYLG	321
Qy	294	VFDIESLVENLLQOLASKQTIILNVVYDITNHSQPISMYGT-NVSAD-GLERSVPLIFGDP	351
Db	322	AFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDFGDP	381
Qy	352	LRKHEMRCRFKQKPPWPVLSMVTSGILVIALLVAHIIHATVSRHKVEEDCDKMQLKK	411
Db	382	FRKHKMICRYHQKAPIPLNLVTTVPFFAIGFLVGIIYGAAMHIVKVEDDFHEMQELKV	441
Qy	412	KAEAADVAKSOFLATVSHEIRTPMNGVLGMLHMLMDTELDVTQQDYVRTAQASGKALVSL	471
Db	442	RAEAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTELSSTQRDYAQTAVCGKALIAL	501
Qy	472	INEVLDOAKIESGKLELEEVRFDLRGILDDVLSFSKSKQKGVVELAVYISDRVPMMLIG	531
Db	502	INEVLDRAKIEAGKLELESVPFDIRSILDVLSLFSESRNKGIELAVFVSDKVPEIVKG	561
Qy	532	DPGRFRQILTNLMGNSIKFTEKGHIFVTVHLVDELPEFIDGETA-----SS	577
Db	562	DSGRFRQIITNLVGNVSKVTEKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQS	621
Qy	578	PESTLSGLPVADRQSRWENFKAFSSNGH--RSFEPSPPDINLIVSVEDTGVGIPVEAQSR	635
Db	622	SYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDIS-SNVRMLVSIEDTIGIGIPLVAQGR	680
Qy	636	IFTPFMQVGPISIRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTTAVFS----	691
Db	681	VFMPFMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDK	740
Qy	692	---NGMQPAERKNDNNQPIFSEFRGMKAVVDHRPARAKVSWHFQRLGIRVEVVRVE	747
Db	741	CSAINHM-----KKPNVEHLPSFTFKGMKAIIVDAKPVRAAVTRHYMKRLGINVDVVTSLK	795
Qy	748	QAL-----HYLKIGT-----TTVNMILIBQEIW--NREADDFIKKLQK----DPLFLSPKL	792
Db	796	TAVVAAAFAERNGSPLPKPKQLDMILVEKDSWISTEDNDSEIRLLNSRTNGNVHHSKSPKL	855
Qy	793	ILLANSVESSISEALCTGIDPPIVIVKPLRASMLAATLQRLGLGIGIREPPQHKGPPALIL	852
Db	856	ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLOQVLELRKTRQHQHEGSSPATL	915
Qy	853	RNLLGRKILIVDDNNVNLRAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQ	912
Db	916	KSLLTGKKILVVDDNIVNRRVAAGALKKFGAEVVCAESGQVALGLLQIPHTFDACFMDIQ	975
Qy	913	MPQMDGFEATPRIRDMEEBEMNKRIKNGEALIVENGNTKSWHLPLVLAMTADVIQATHEECL	972
Db	976	MPQMDGFEATPRQIRMMEKEAKEK-----TNLEWHLPLAMTADVIHATYEACL	1023
Qy	973	KCGMDGYVSKPFEAEQLYREVSRFFN-----SPS 1001	

Db	1024	KSGMDGYVSKPFEENLYKSVAKSFKNPISPS 1056	
RESULT 11			
US-10-135-322-5			
; Sequence 5, Application US/10135322			
; Publication No. US20020173017A1			
; GENERAL INFORMATION:			
; APPLICANT: BENFEY, PN			
; APPLICANT: HELARIUTTA, Y			
; APPLICANT: MAHONEN, AP			
; APPLICANT: BONKE, AWM			
; APPLICANT: KAUPPINEN, L			
; APPLICANT: RIIKONEN, M			
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF			
; FILE REFERENCE: 5914-086-999			
; CURRENT APPLICATION NUMBER: US/10/135,322			
; CURRENT FILING DATE: 2002-04-30			
; PRIOR APPLICATION NUMBER: 60/253,739			
; PRIOR FILING DATE: 2000-11-29			
; NUMBER OF SEQ ID NOS: 43			
; SOFTWARE: PatentIn version 3.0			
; SEQ ID NO 5			
; LENGTH: 1057			
; TYPE: PRT			
; ORGANISM: Arabidopsis thaliana			
US-10-135-322-5			
Query Match 48.0%; Score 2475.5; DB 14; Length 1057;			
Best Local Similarity 50.8%; Pred. No. 2.1e-214;			
Matches 535; Conservative 156; Mismatches 251; Indels 111; Gaps 18;			
Qy	21	MTTLKKKNKMFWNKISSSGLKIPSPS-----YQFLGSVKFN-----	57
Db	43	LNSSEKPRKIDFWR----SGLM--GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTF	96
Qy	58	----KAWWRKLVVVVWVFWVLVSIWTFWYFSSQAMEKREKETLASMCDERARMLQDQFNVS	113
Db	97	IQEHRALLPKALILWIIIVGFISSGIYQWMDANKIRREEVLSVMSCDQARMLQDQFSVS	156
Qy	114	MNHVQAMSIISTFHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEEFE	173
Db	157	VNHVHALAILVSTFHYHKNPSAIDQETFAEYTARTAFERPLLSGVAYAEKVNFEREMFE	216
Qy	174	RQCGWTIRKMYSLEQNPFVKDDYDLEALEPSPVQEEYAPVIFAQDTSVSHVSLDMLSGKE	233
Db	217	RQHNWVIKTM-----DRGEPSVRDEYAPVIFSQDSVSYLESLDMMSGEE	261
Qy	234	DRENVLRARSSGKGVLTAPPPLIKTNRLGVILTFVAVYKRDLPSPNATPKERIEATNGYLG	293
Db	262	DRENILRARETGKAVLTSPFRLLETHHLGVLTFFPVYKSSLPENPTVEERIAATAGYLG	321
Qy	294	VFDIESLVENLLQOLASKQTIILNVVYDITNHSQPISMYGT-NVSAD-GLERSVPLIFGDP	351
Db	322	AFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDFGDP	381
Qy	352	LRKHEMRCRFKQKPPWPVLSMVTSGILVIALLVAHIIHATVSRHKVEEDCDKMQLKK	411
Db	382	FRKHKMICRYHQKAPIPLNLVTTVPFFAIGFLVGIIYGAAMHIVKVEDDFHEMQELKV	441
Qy	412	KAEAADVAKSOFLATVSHEIRTPMNGVLGMLHMLMDTELDVTQQDYVRTAQASGKALVSL	471
Db	442	RAEAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTELSSTQRDYAQTAVCGKALIAL	501
Qy	472	INEVLDOAKIESGKLELEEVRFDLRGILDDVLSFSKSKQKGVVELAVYISDRVPMMLIG	531
Db	502	INEVLDRAKIEAGKLELESVPFDIRSILDVLSLFSESRNKSIELAVFVSDKVPEIVKG	561
Qy	532	DPGRFRQILTNLMGNSIKFTEKGHIFVTVHLVDELPEFIDGETA-----SS	577
Db	562	DSGRFRQIITNLVGNVSKVTEKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQS	621
Qy	578	PESTLSGLPVADRQSRWENFKAFSSNGH--RSFEPSPPDINLIVSVEDTGVGIPVEAQSR	635

Db 622 SYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDIS-SNVRMLVMSIEDTGIGIPLVAQGR 680
QY 636 IFTPFMVGPSISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTTAVFS---- 691
Db 681 VFMPFMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDK 740
QY 692 ----NGMQPAERKNDNNQPIFSEFRGMKAVVDHRPARAKVSWYHFQRLGIRVEVVRVE 747
Db 741 CSAINHM-----KKPNVEHLPSFTFKGMKAIVDAKPVRAAVTRYHMKRLGINVDVVTSLK 795
QY 748 QAL-----HYLKIGT-----TTVNMILIEQEIW--NREADDFIKKLQK----DPLFLSPKL 792
Db 796 TAVVAAAAFERNGSPLPTKPQLDMILVEKDSWISTEDNDSEIRLLNSRTNGNVHHKSPKL 855
QY 793 ILLANSVSESSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIREPPQHKGPALIL 852
Db 856 ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELRKTRQOHPEGSSPATL 915
QY 853 RNLLGRKILIVDDNNVLRVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQ 912
Db 916 KSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCAESGQVALGLLQIPHTFDACFMDIQ 975
QY 913 MPMDGFEATRIRDMEEEMNKRIKNGEALIVENGKNTSWHLPLVAMTADVIQATHEECL 972
Db 976 MPQMDGFEATRQIRMMEKETKEK-----TNLEWHLPILAMTADVIHATYEEL 1023
QY 973 KCGMDGYVSKPFEAEQLYREVSRFFN----SPS 1001
Db 1024 KSGMDGYVSKPFEENLYKSAKSFKNPISPS 1056

RESULT 12

US-10-135-322-24
; Sequence 24, Application US/10135322
; Publication No. US20020173017A1
; GENERAL INFORMATION:
; APPLICANT: BENFEY, PN
; APPLICANT: HELARIUTTA, Y
; APPLICANT: MAHONEN, AP
; APPLICANT: BONKE, AWM
; APPLICANT: KAUPPINEN, L
; APPLICANT: RIIKONEN, M
; TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
; FILE REFERENCE: 5914-086-999
; CURRENT APPLICATION NUMBER: US/10/135,322
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/253,739
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
; LENGTH: 1057
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-135-322-24

Query Match 48.0%; Score 2475.5; DB 14; Length 1057;
Best Local Similarity 50.8%; Pred. No. 2.1e-214;
Matches 535; Conservative 156; Mismatches 251; Indels 111; Gaps 18;

QY 21 MTTLKKKNKMFNWKISSGLKIPSF-----YQFLGSVKFN----- 57
Db 43 LNSSEKPRKIDFWR---SGLM--GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTF 96
QY 58 ----KAWRKLVVVWVFWVLVSIWTFWYFSSQAMEKRKETLASMCDERARMQLQDFNVS 113
Db 97 IQEHRALLPKALILWIIIVFISSGIYQWDDANKIRREEVLVSMCDQARMQLQDFSVS 156
QY 114 MNHVQAMSILSTFHHGKIPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEREEFE 173
Db 157 VNHVHALAILVSTFHYHKNPSAIDQETFAEYRTARTAFERPLLSGVAYAEKVVNFEREMFE 216

QY 174 RQQGWTIKMYSLQNPVHKDDYDLEALEPSPVQEEYAPVIFAQDTSVSHVSLDMLSGKE 233
Db 217 ROHNWVIKTM-----DRGEPSPVDRDEYAPVIFSQDSVSYLESJLDMMSGEE 261
QY 234 DRENVLRARSSGKGLTAPFPPLIKTNRLGVILTFAVYKRDLPNSNATPKERIEATNGYLG 293
Db 262 DRENILRARETGKAVLTSPFRLLETHHLGVVLTFFPVYKSSLPENPTVEERIAATAAGYLG 321
QY 294 VFDIESLVENLLQOLASKQITILNVYDITNHSQPISMYGT-NVSAD-GLERSVPLIFGDP 351
Db 322 AFDVESLVENLLGOLAGNQAIVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDFGDP 381
QY 352 LRKHEMRCRFKQKPPWPVLSMVTSPGILVIALLVAAHIIHATVSRHKKVEEDCDKMKQLKK 411
Db 382 FRKHKMICRYHOKAPIPLNVLTTPVPLFAIGFLVGYILYGAAMHIVKVEDDFHEMQELKV 441
QY 412 KAEAADVAKSQFLATVSHSIRTPMNGVLGMLHMLMDTELDTQDQYVRTAQASGKALVSL 471
Db 442 RAEAADVAKSQFLATVSHSIRTPMNGILGMLAMLDTLSTQDYAQTAQVCGKALIAL 501
QY 472 INEVLDAQIESGKLEBEVFRDLRGILDVLSLFSSKSOQKGVELAVYISDRVPDMLIG 531
Db 502 INEVLDRAKTEAGKLELESVPFDIRSILDVLSLFSESRNKSIELAVFVSDKVPEIVKG 561
QY 532 DPGRRQIILTNLMGNSIKFTEKGHIFVTVHLVDELPEFESIDGETA-----SS 577
Db 562 DSGRRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDESEPKNALNGVSEEMIVVSKQS 621
QY 578 PESTLSGLPVADRQSRWENFKAFSSNGH--RSFEPSPDINLIVSVEDTGVGIPVEAQSR 635
Db 622 SYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDIS-SNVRMLVMSIEDTGIGIPLVAQGR 680
QY 636 IFTPFMVGPSISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTTAVFS---- 691
Db 681 VFMPFMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDK 740
QY 692 ----NGMQPAERKNDNNQPIFSEFRGMKAVVDHRPARAKVSWYHFQRLGIRVEVVRVE 747
Db 741 CSAINHM-----KKPNVEHLPSFTFKGMKAIVDAKPVRAAVTRYHMKRLGINVDVVTSLK 795
QY 748 QAL-----HYLKIGT-----TTVNMILIEQEIW--NREADDFIKKLQK----DPLFLSPKL 792
Db 796 TAVVAAAAFERNGSPLPTKPQLDMILVEKDSWISTEDNDSEIRLLNSRTNGNVHHKSPKL 855
QY 793 ILLANSVSESSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIREPPQHKGPALIL 852
Db 856 ALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELRKTRQOHPEGSSPATL 915
QY 853 RNLLGRKILIVDDNNVLRVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQ 912
Db 916 KSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCAESGQVALGLLQIPHTFDACFMDIQ 975
QY 913 MPMDGFEATRIRDMEEEMNKRIKNGEALIVENGKNTSWHLPLVAMTADVIQATHEECL 972
Db 976 MPQMDGFEATRQIRMMEKETKEK-----TNLEWHLPILAMTADVIHATYEEL 1023
QY 973 KCGMDGYVSKPFEAEQLYREVSRFFN----SPS 1001
Db 1024 KSGMDGYVSKPFEENLYKSAKSFKNPISPS 1056

RESULT 13

US-10-126-120-2
; Sequence 2, Application US/10126120
; Publication No. US20030108526A1
; GENERAL INFORMATION:
; APPLICANT: Sakakibara, Hitoshi
; APPLICANT: Takei, Kentaro
; TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FACTS
; FILE REFERENCE: 11127-004001
; CURRENT APPLICATION NUMBER: US/10/126,120
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: JP 2001-291059

```
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Zea mays
US-10-126-120-2

Query Match          47.7%; Score 2462; DB 15; Length 974;
Best Local Similarity 51.8%; Pred. No. 3e-213;
Matches 512; Conservative 161; Mismatches 246; Indels 70; Gaps 14;

Qy 58 KAWRKLVVV-WVFWVLVSIWTFWYFSSQAMEKRKETLASMCDERARMLQDQFNVMNH 116
Db 11 KRWRGLAAGWVLTAVVCSAVMHWTLRRDSMDRAEERLVSMCEERARMLOEQFGVTVNH 70

Qy 117 VQAMSIILSTFHGKIPSAIDQRTSEYTDRTSFERPLTSGVAYAMRVLHSEREEFERQQ 176
Db 71 VHAIALISTFNFEKSPPAIDQDTFAKYTARTSFERPLLNGVAFARVFHHEREMFESQQ 130

Qy 177 GWTIRKMYSLQNPNVHKDDYDLEALEPSPVQEEYAPVIFAQDVTSHVVSLDMLSGKEDRE 236
Db 131 GWVMTNMQR-----EPAPPQVEYAPVIFSQDTSYLARIDMMSGEEDRE 174

Qy 237 NVLRARSSGKGVLTAPFPLIKTNRLGVILTFFAVYKRDLPNSATPKERIEATNGYLGVPD 296
Db 175 NIFRARTTGKAVLTNPFRLLGSHNLGVLTFAVYRPDLPADASVEQRVEATIGYLGAFD 234

Qy 297 IESLVENLLQOLASKQTILNVVYDITNHSQPISMYGTNVSADGLE--RVSPLIFGDPLRK 354
Db 235 VESLVENLLSKLAGNQDIVNVVYDVTNASDAMVLYGPSSLDEQVFFLHVSMLDGDPFRK 294

Qy 355 HEMRCRFKQKPPWPVLSMVTSEFGLIVIALIVAHIIHATVSRHKEVEDCDKMKQLKKKAE 414
Db 295 HEMRCRYRQKLPMPWSAITNPGLGTFVIWMLLGYISAAAYSRYDKVTEDCRKMEELKTQAE 354

Qy 415 AADVAKSQFLATVSHEIRTPMNGVLGMLHMLMDTDLDTQDQYVRTAQASGKALVSLINE 474
Db 355 AADVAKSQFLATASHEIRTPMNGVLGMLDMLLGTDLTMTQXDYAQTQACMGRALITLND 414

Qy 475 VLDQAKIESGKLELEEVRFDLRGILDVLSLFSSKSKQKGVELAVYISDRVPDMLIGDPG 534
Db 415 VLDRAKIEAGKLELEAVPFDRLSLMDDVVSFLFSSKSKREKCIELAVFVCDNVKVVIGDPW 474

Qy 535 RFRQILTNLMGNSIKFTEKGHIFVTVHLVDE-----LFESIDGE-----TASSPES 580
Db 475 RFRQILTNLVGNNAVKFTERGHVFRVCLAENSNMEANQVLHGAMNGKGRVESTANGAPN 534

Qy 581 TLGSLPVADRQRSWENKFAFSSN-----GHRSPFSPPPDINLIVSVEDTGVGIPVE 631
Db 535 TLSGFEAADRRNSWQYFKLLSDKESLLDDLESENSNQSDSDRVTLAISIEDTGVGIPLQ 594

Qy 632 AQSRITPFMQVGPSISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTFTAVFS 691
Db 595 AQDRVTFPMQADSSTSRNYGGTGIGLSISKCLAEALMGGOISFTSHPSVSGSTFTFSATLK 654

Qy 692 NGMQ--PAERKNDNNQPIFSEFRGMKAVVVDHRRPARAKVSWHFQRLGIRVEVVRVBEQA 749
Db 655 HSHKDISGSSRSRLTEALPTAFKGMKAILVDGRPVRSVAVRYHLKRLGILLQVVNNMNAV 714

Qy 750 LHYL-----KIGT-TTVNMILIEQEIWNREAD----DFIKLQKDPLFLSPKLIILANSV 799
Db 715 VKAFPQNGAAGSREKASILFIESDFWRPETHVQVLLNHLREQNQLSDGHKVVLLVTSE 774

Qy 800 E-----SSISEALCTGIDPPIVIVKPLRASMLAATLQRLGIGIGIREPPQHKGPALILRN 854
Db 775 ADKDKYGSIFD-----IVMCKPIRASTIASIIQQLLVKVEIAERKDNQNRPS-FLRS 824

Qy 855 LLLGRKILIVDDNNVNLRVAAGALKKYGADVVCAESGIKAISSLKPPHEFDACFMDIQMP 914
Db 825 LLVGKNILVVDDNKVNLRVAAALKKYGANVSCVESGKDAISLLQPPHFRFDACFMDVQMP 884
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Qy 915 EMDGFEATRRIRDMEEMNKRIKNGEALIVENGKNTSWHLPVLTAMTADVIQATHEECIKC 974
Db 885 EMDGFEATGQIRQMELKANEERKNKLASI-EGSTTAEVHLPVLTAMTADVIQATYEECIKS 943

Qy 975 GMDGYVSKPFEAEQLYREVSRFFNFSPSDT 1003
Db 944 GMDGYVSKPFDEEQLYQAVSRLVVGTTDS 972

RESULT 14
US-10-101-464A-978
; Sequence 978, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 978
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-978

Query Match          26.5%; Score 1368.5; DB 15; Length 480;
Best Local Similarity 59.2%; Pred. No. 9.3e-115;
Matches 277; Conservative 72; Mismatches 98; Indels 21; Gaps 3;

Qy 48 YQFLGSVKFNKAWRKLVVVWVFWVLVSIWTFWYFSSQAMEKRKETLASMCDERARMLQ 107
Db 26 YTFIQS---NRAWIPKILVLSVVGMAFLSMSIYRKMDADIKVRRKEVLVSMCDQARMLK 82

Qy 108 DQFNVMNHVQAMSIILSTFHGKIPSAIDQRTSEYTDRTSFERPLTSGVAYAMRVLHS 167
Db 83 DQFSVSVNHVHALAILVSTFHYKPNPSAIDQETFAEYRTARTAFERPLLSGVAYAEVRTNS 142

Qy 168 EREEFERQGGWTIRKMYSLQNPNVHKDDYDLEALEPSPVQEEYAPVIFAQDVTSHVVSLD 227
Db 143 EREKFEEQHGWITIKMEK-----QSPVPRDEYAPVIFSQETVSYIESLD 186

Qy 228 MLSGKEDRENVLRRSSGKGVLTAPFPLIKTNRLGVILTFFAVYKRDLPNSATPKERIEAT 287
Db 187 MMSGEEDRENILRARATGKAVLTSPFRLLGSHHLGVLTFFPVYKSLPPNPVTVEERIEAT 246

Qy 288 NGYLGGVFDIESLVENLLQOLASKQTILNVVYDITNHSQPISMYGTNUSA--DGLERVSP 345
Db 247 VGYLGGAFDVESLVENLLQOLDGNQAILNVVYDVTNNSSEPLIMYGHQYQECDTSLHESK 306

Qy 346 LIFGDPPLRKHEMRRCRFKQKPPWPVLSMVTSEFGLIVIALIVAHIIHATVSRHKEVEDCDK 405
Db 307 LDFGDPFRKHQMICYHYQKAPPSWTALTTAFFVFIGLLVGVIYLYGAATHIVKVEDDDFHE 366

Qy 406 MKQLKKKAAEADVAKSQFLATVSHEIRTPMNGVLGMLHMLMDTDLDTQDQYVRTAQASG 465
Db 367 MQELKVRAEADVAKSQFLATVSHEIRTPMNGILGMLALLDTELSSTQRDYAQTQICG 426

Qy 466 KALVSLINEVLDQAKIESGKLEEEVRFDLRGILDVLSLFSSKSKQK 513
Db 427 KALIALINEVLDRAKIEAGKLELETVPFDIRSIILDDVLSLFSEESRHK 474
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Job time : 30.7424 secs

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RESULT 15
US-10-101-464A-955
; Sequence 955, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-955
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```
Query Match      20.2%; Score 1041; DB 15; Length 482;
Best Local Similarity 47.1%; Pred. No. 4.2e-85;
Matches 230; Conservative 76; Mismatches 130; Indels 52; Gaps 11;

QY 555 HIFVTVHLVDLPESIDGETAS----SPE-----STLSGLPVADRQRSWENFKA 599
Db 1 HIFVKVHLADQVKGATNAHAKTCLNGRPEEDILISDGSHLETLSGCEVADERNSWDTFNL 60

QY 600 F-----SSNGHRSEFPSPDINLIVSVEDTGIGIPVEAQSRIFTPFMQVGPSISRTHG 652
Db 61 LVAEDQFNVSVDNMTSNEASENVTVMVSVEDTGIGIPLRAQDRVFMPFQADSSTSRTYG 120

QY 653 GTGIGLSISKCLVGLMKGEIGFSSTPKVGSTFTTAVFSGMGQPAERKNDNN-----QPI 707
Db 121 GTGIGLSISKCLVELMGHINFISRPQIGSTFSTAVFGR----CKRLVFANVKRTFEDL 176

QY 708 FSEFRGMKAVVVDHPRAPAKVSWYHFQRLGIRVEVVPRVEQAL-----HYLKIGITTVN 761
Db 177 PSGFKGLKAIVVVGKPVRAAVTRYHLNRLGINVEVASSINAITATGGKNGSLTAGYRHPD 236

QY 762 MILIEQEIWNREADDFIKKL-----QKDPLFLSPKLIILLANSVSESSISEALCTGIDPPIV 816
Db 237 IILVEKDMMSIDSWISLTVADWKQNGNLIQLPKILLASKISASELEKAKASGF-ADTV 295

QY 817 IVKPLRASMLAATLQRLGIGIGIREPPQ-----HKGPPALILRNLLGRKILIVDDNNVNL 871
Db 296 IMKPVRASMLAACLQQVLGIGRKKQLQKDMNMRNGSSA--LRSLLYGKKILVVDDNKVNR 353

QY 872 RVAAGALKKYGADVCAESGIKAISLLKPPHEFDACFMDIQMPMDGFEATRIRDMEEE 931
Db 354 RVAAGALKKFGANVECAESGKALELLQLPHDFACFMDIQMPMDGFEATRQIRLMESQ 413

QY 932 MNKRIKNGEALIVENGKNTSWHLPLVAMTADVIQATHEECLKCGMDGYVSKPFEAEQLYR 991
Db 414 VNEQMKSESAVQIVKGE--WHMPILAMTADVIHATYDECLKCGMDGYVSKPFDDEENLYQ 471

QY 992 EVSRFFNS 999
Db 472 AVAKFFRT 479
```

Search completed: November 28, 2003, 14:08:39

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:54 ; Search time 35.4302 Seconds
(without alignments)
7698.569 Million cell updates/sec

Title: US-09-918-508-6
Perfect score: 5397
Sequence: 1 MNWALNNHQEEEEPRRIE1.....ENLYKSVAKSFKNPISPSS 1057

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_23.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertibrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5397	100.0	1057	10 Q9C5T9	Q9c5t9 arabidopsis
2	5397	100.0	1080	10 Q9C5T8	Q9c5t8 arabidopsis
3	5387	99.8	1057	10 Q9S1T0	Q9s1t0 arabidopsis
4	5387	99.8	1080	10 Q9C5U0	Q9c5u0 arabidopsis
5	2705.5	50.1	974	10 Q9FRY7	Q9fry7 zea mays (m
6	2546	47.2	1176	10 Q9C5U2	Q9c5u2 arabidopsis
7	2534.5	47.0	1173	10 Q9FKH3	Q9fkh3 arabidopsis
8	2485	46.0	1036	10 Q9C5U1	Q9c5u1 arabidopsis
9	2431.5	45.1	1041	10 Q8L8I6	Q8l8i6 catharanthu
10	2402	44.5	1092	10 Q9FZK3	Q9fzk3 arabidopsis
11	2375	44.0	1023	10 Q8RYG4	Q8ryg4 oryza sativ
12	2248.5	41.7	925	10 Q8S6P5	Q8s6p5 oryza sativ
13	1698.5	31.5	652	10 Q8GUG0	Q8gu0 arabidopsis
14	1042	19.3	627	10 Q9AUQ0	Q9auq0 oryza sativ
15	806.5	14.9	1765	16 Q8E1I0	Q8ei0 shewanella
16	792.5	14.7	1268	2 Q8KQV0	Q8kqv0 vibrio chol

17	790.5	14.6	1261	16 P73926	P73926 synechocyst
18	785	14.5	1364	16 Q8PJN8	Q8pjn8 xanthomonas
19	777	14.4	1462	16 P73035	P73035 synechocyst
20	772.5	14.3	1417	16 Q9HWR8	Q9hwr8 pseudomonas
21	771.5	14.3	1550	16 Q8YQQ8	Q8yqq8 anabaena sp
22	767.5	14.2	1353	16 Q8DJE3	Q8dje3 synechococc
23	764.5	14.2	2062	5 Q95PH6	Q95ph6 dictyosteli
24	757	14.0	928	16 Q8DC68	Q8dc68 vibrio vuln
25	752.5	13.9	1364	16 Q8P883	Q8p883 xanthomonas
26	750.5	13.9	1299	16 Q8YUQ6	Q8yuq6 anabaena sp
27	740	13.7	1035	16 Q8DKI3	Q8dki3 synechococc
28	729.5	13.5	1331	16 Q9KSB0	Q9ksb0 vibrio chol
29	726.5	13.5	1320	16 Q8D5E0	Q8d5e0 vibrio vuln
30	726	13.5	918	16 Q8Z445	Q8z445 salmonella
31	725	13.4	918	16 Q9L9E4	Q9l9e4 salmonella
32	725	13.4	1188	16 Q8EJ91	Q8ej91 shewanella
33	721	13.4	1817	16 Q8YT51	Q8yt51 anabaena sp
34	717	13.3	928	2 O32556	O32556 pectobacter
35	715.5	13.3	786	16 Q98FG5	Q98fg5 rhizobium 1
36	708.5	13.1	908	2 Q8GMB7	Q8gmb7 pantoea agg
37	707	13.1	927	16 Q9KPC0	Q9kpc0 vibrio chol
38	704	13.0	925	16 O31138	O31138 pseudomonas
39	702	13.0	2150	5 Q23863	Q23863 dictyosteli
40	695.5	12.9	929	2 O08235	O08235 pectobacter
41	695.5	12.9	1391	16 Q98FL1	Q98fl1 rhizobium 1
42	693.5	12.8	919	16 Q9HYE4	Q9hye4 pseudomonas
43	692.5	12.8	935	2 Q8RMF4	Q8rmf4 acinetobact
44	685	12.7	917	2 Q9ZNQ1	Q9znq1 pseudomonas
45	685	12.7	929	16 Q8EBQ2	Q8ebq2 shewanella

ALIGNMENTS

RESULT 1

Q9C5T9 ID Q9C5T9 PRELIMINARY; PRT; 1057 AA.

AC Q9C5T9;

DT 01-JUN-2001 (TRENBLrel. 17, Created)

DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)

DE Cytokinin receptor CRE1a.

GN CRE1.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Wassilewskija;

RA Inoue T., Higuchi M., Hashimoto Y., Seki M., Kobayashi M., Kato T.,

RA Satoshi T., Shinozaki K., Kakimoto T.;

RT "Identification of a cytokinin receptor, CRE1, from Arabidopsis.";

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB049934; BAB33310.1; -.

DR HSSP; P06657; 2CHF.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW	Phosphorylation; Receptor; Sensory transduction.									
SQ	SEQUENCE 1057 AA; 117894 MW; E121A86345F0C292 CRC64;									
	Query Match	100.0%;	Score 5397;	DB 10;	Length 1057;					
	Best Local Similarity	100.0%;	Pred. No. 0;							
	Matches 1057;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;					
Qy	1	MNWALNNHQEEEEPRRIEISDSSELENLKSSDFYQLGGGALNSSEKPRKIDFWRSGLM	60							
Db	1	MNWALNNHQEEEEPRRIEISDSSELENLKSSDFYQLGGGALNSSEKPRKIDFWRSGLM	60							
Qy	61	GFAKMQQQQLQHSVAVKMNNNNNNDLMGNKKGSTFIQEHRAALLPKALILWIIIVGFISS	120							
Db	61	GFAKMQQQQLQHSVAVKMNNNNNNNNDLMGNKKGSTFIQEHRAALLPKALILWIIIVGFISS	120							
Qy	121	GIYQWMDANKIRREEVLVSMCDQARMLQDQFSVSNVHVHALAILVSTFHYHKNPSAID	180							
Db	121	GIYQWMDANKIRREEVLVSMCDQARMLQDQFSVSNVHVHALAILVSTFHYHKNPSAID	180							
Qy	181	QETFAEYTARTAFERPLLSGVAYAEKVVNFEREMFERQHNWVIKTMDRGEPSPVRDEYAP	240							
Db	181	QETFAEYTARTAFERPLLSGVAYAEKVVNFEREMFERQHNWVIKTMDRGEPSPVRDEYAP	240							
Qy	241	VIFSQDSVSYLESDDMSGEEDRENILRARETGKAVLTSPFRLETHHLGVLTFFPVYKS	300							
Db	241	VIFSQDSVSYLESDDMSGEEDRENILRARETGKAVLTSPFRLETHHLGVLTFFPVYKS	300							
Qy	301	SLPENPTVEERIAATAGYLGGAADFVESILVENLLGQLAGNQAIVVHVYDITNASDPLVMYG	360							
Db	301	SLPENPTVEERIAATAGYLGGAADFVESILVENLLGQLAGNQAIVVHVYDITNASDPLVMYG	360							
Qy	361	NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTVPLFFAIGFLVGYYLY	420							
Db	361	NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTVPLFFAIGFLVGYYLY	420							
Qy	421	GAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHEIRTPMNGILGMLAMDTEL	480							
Db	421	GAAMHIVKVEDDFHEMQELKVRAEADVAKSQFLATVSHEIRTPMNGILGMLAMDTEL	480							
Qy	481	SSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLESVFPDIRSILDDVLSLFSEES	540							
Db	481	SSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLESVFPDIRSILDDVLSLFSEES	540							
Qy	541	RNKGIELAVFVSDKVEIIVKGDGSRFRQIILNLVGNVVKFTEKGHIFVKVHLAEQSKDES	600							
Db	541	RNKGIELAVFVSDKVEIIVKGDGSRFRQIILNLVGNVVKFTEKGHIFVKVHLAEQSKDES	600							
Qy	601	EPKNALNGVSEEMIVVSKOSSYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDISSNV	660							
Db	601	EPKNALNGVSEEMIVVSKOSSYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDISSNV	660							
Qy	661	RLMVSIEDTGIGIPLVAQGRVFMPEMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI	720							
Db	661	RLMVSIEDTGIGIPLVAQGRVFMPEMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI	720							
Qy	721	SRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPSTFTKGMKAIVVDAKPVRAAVTRYH	780							
Db	721	SRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPSTFTKGMKAIVVDAKPVRAAVTRYH	780							
Qy	781	MKRLGINVDVVTSLKTAVVAAAFAFERNGSPLTPKPQLDMILVEKDSWISTEDNDSEIRLL	840							
Db	781	MKRLGINVDVVTSLKTAVVAAAFAFERNGSPLTPKPQLDMILVEKDSWISTEDNDSEIRLL	840							
Qy	841	NSRTNGNVHHKSPKALFATNITNSEFDRAKSAGFADTVIMKPLRASWIGACLQQVLELR	900							
Db	841	NSRTNGNVHHKSPKALFATNITNSEFDRAKSAGFADTVIMKPLRASWIGACLQQVLELR	900							
Qy	901	KTRQQHPEGSSPATLSLLTGKILVVDDNIVNRRVAAGALKKFGAEVVCAESGQVALGL	960							
Db	901	KTRQQHPEGSSPATLSLLTGKILVVDDNIVNRRVAAGALKKFGAEVVCAESGQVALGL	960							
Qy	961	LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKEAKEKTNLEWHLPILAMTADVIHATYE	1020							

Ddb	961	LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKEAKEKTNLEWHLPILAMTADVIHATYE	1020																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
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Db 264 VIFSQDSVSYLESIDMMSGEEDRENILRARETGKAVLTSPFRLLLETHLGVVLTFFPVYKS 323

QY 301 SLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNQAIWVHYDITNASDPLVMYG 360

Db 324 SLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNQAIWVHYDITNASDPLVMYG 383

QY 361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTPVLFFAIGFLVGILY 420

Db 384 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTPVLFFAIGFLVGILY 443

QY 421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480

Db 444 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 503

QY 481 SSTQDYAQTAVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540

Db 504 SSTQDYAQTAVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 563

QY 541 RNKGIELAVFVSDKVPETVKGDSGRFRQIIINLVGNSVKFTEKGHIFVKVHLABQSKDES 600

Db 564 RNKGIELAVFVSDKVPETVKGDSGRFRQIIINLVGNSVKFTEKGHIFVKVHLABQSKDES 623

QY 601 EPKNALNGGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660

Db 624 EPKNALNGGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 683

QY 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNVGGTGIGLSISKCLVELMRGQINFI 720

Db 684 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNVGGTGIGLSISKCLVELMRGQINFI 743

QY 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLESTFKGMKAIIVDAKPVRAAVTRYH 780

Db 744 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLESTFKGMKAIIVDAKPVRAAVTRYH 803

QY 781 MKRLGINVDVVTSLKTAVVAAAAFERNGSPLPKPKQLDMILVEKDSWISTEDNDSEIRLL 840

Db 804 MKRLGINVDVVTSLKTAVVAAAAFERNGSPLPKPKQLDMILVEKDSWISTEDNDSEIRLL 863

QY 841 NSRTNGNVHKSPLKALFATNITNSEFDRAKSAGFADTVIMKPLRASMGACIQQVLELR 900

Db 864 NSRTNGNVHKSPLKALFATNITNSEFDRAKSAGFADTVIMKPLRASMGACIQQVLELR 923

QY 901 KTRQOHPEGSSPATLKSLLTGKKILVVDDNIVNRRVAAGALKKFGAEVVCAESGQVALGL 960

Db 924 KTRQOHPEGSSPATLKSLLTGKKILVVDDNIVNRRVAAGALKKFGAEVVCAESGQVALGL 983

QY 961 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKEAKBKTNLEWHLPILAMTADVIHATYE 1020

Db 984 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKEAKBKTNLEWHLPILAMTADVIHATYE 1043

QY 1021 ECLKSGMDGYVSKPFEENLYKSVAKSFKNPISPSS 1057

Db 1044 ECLKSGMDGYVSKPFEENLYKSVAKSFKNPISPSS 1080

RESULT 3

Q9SIT0

ID Q9SIT0 PRELIMINARY; PRT; 1057 AA.

AC Q9SIT0; Q9FD23;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Putative histidine kinase (Putative histidine kinase receptor).

GN AT2G01830 OR WOL.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,

RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,

RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,

RA Fraser C.M., Venter J.C.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBDJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Root;

RX PubMed=11114883;

RA Mahonen A., Bonke M.A., Kauppinen L., Riikonen M., Benfey P.N.,

RA Helariutta Y.;

RT ~~A novel two component hybrid molecule regulates the vascular pattern~~

RT ~~of the Arabidopsis root.~~;

RL Genes Dev. 14:2938-2943 (2000).

DR EMBL; AC007069; AAD21777.2; -.

DR EMBL; AJ278530; CAC18523.1; -.

DR EMBL; AJ278528; CAC18521.1; -.

DR EMBL; AJ278529; CAC18522.1; -.

DR HSSP; P06143; 1D4Z.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR004358; Bact_sens_pr_C.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR PRINTS; PR00344; BCTRLSENSOR.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW Kinase; Phosphorylation; Receptor; Sensory transduction.

SQ SEQUENCE 1057 AA; 117954 MW; E1381C8685F0D787 CRC64;

Query Match 99.8%; Score 5387; DB 10; Length 1057;

Best Local Similarity 99.8%; Pred. NO. 0;

Matches 1055; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNWALNNHQEEEEPRRIEISDSELENLKSSDFYQLGGGALNSSEKPKIDFWRSGLM 60

Db 1 MNWALNNHQEEEEPRRIEISDSELENLKSSDFYQLGGGALNSSEKPKIDFWRSGLM 60

QY 61 GFAKMQQQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFSS 120

Db 61 GFAKMQQQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFSS 120

QY 121 GIYQWMDANKIRREEVLVSMCDQARMLQDQFSVSNHVHALAILVSTFHYHKNPSAID 180

Db 121 GIYQWMDANKIRREEVLVSMCDQARMLQDQFSVSNHVHALAILVSTFHYHKNPSAID 180

QY 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240

Db 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240

QY 241 VIFSQDSVSYLESIDMMSGEEDRENILRARETGKAVLTSPFRLLLETHLGVVLTFFPVYKS 300

Db 241 VIFSQDSVSYLESIDMMSGEEDRENILRARETGKAVLTSPFRLLLETHLGVVLTFFPVYKS 300

QY 301 SLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNQAIWVHYDITNASDPLVMYG 360

Db 301 SLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNQAIWVHYDITNASDPLVMYG 360

QY 361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTPVLFFAIGFLVGILY 420

Db 361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTPVLFFAIGFLVGILY 420

QY 421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480

Db 421 GAAMHIVKVEDDFHEMQELKVRAEAADVAKSQFLATVSHSHEIRTPMNGILGMLAMDTEL 480

QY 481 SSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540

Db 481 SSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540

QY 541 RNKGIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600

Db 541 RNKSIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600

QY 601 EPKNALNGGVSEEMIVWSKQSSYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660

Db 601 EPKNALNGGVSEEMIVWSKQSSYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660

QY 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSTSRNYGGTGIGLSISKCLVELMRGQINF1 720

Db 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSTSRNYGGTGIGLSISKCLVELMRGQINF1 720

QY 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKKNVEHL PSTFKGMKAI VVDKPVRAAVTRYH 780

Db 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKKNVEHL PSTFKGMKAI VVDKPVRAAVTRYH 780

QY 781 MKRLGINVDVVTSLKTAVVAAAFAERNGLPTKPKQLDMILVEKDSWISTEDNDSEIRLL 840

Db 781 MKRLGINVDVVTSLKTAVVAAAFAERNGLPTKPKQLDMILVEKDSWISTEDNDSEIRLL 840

QY 841 NSRTNGNVHHKSPKALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELR 900

Db 841 NSRTNGNVHHKSPKALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELR 900

QY 901 KTRQOHPEGSSPATLSLLTGKILVDDNIVNRRVAAGALKKFGAEVYCAESGQVALGL 960

Db 901 KTRQOHPEGSSPATLSLLTGKILVDDNIVNRRVAAGALKKFGAEVYCAESGQVALGL 960

QY 961 LQIPHTFDACFMDIQMPQMDGFEATQIRNMEKEAKEKTNLEWHLPILAMTADVIHATYE 1020

Db 961 LQIPHTFDACFMDIQMPQMDGFEATQIRNMEKEAKEKTNLEWHLPILAMTADVIHATYE 1020

QY 1021 ECLKSGMDGYVSKPFEENLYKSVAKSKFKNPISPSS 1057

Db 1021 ECLKSGMDGYVSKPFEENLYKSVAKSKFKNPISPSS 1057

RESULT 4

Q9CSU0 PRELIMINARY; PRT; 1080 AA.

ID Q9CSU0

AC Q9CSU0

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Histidine kinase.

GN AHK4.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21154803; PubMed=11230578;

RA Ueguchi C., Koizumi H., Suzuki T., Mizuno T.;

RT "Novel family of sensor histidine kinase genes in Arabidopsis thaliana.";

RL Plant Cell Physiol. 42:231-235(2001).

DR EMBL; AB046871; BAB40776.1; -.

DR HSSP; P06657; 2CHF.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW Kinase; Phosphorylation; Sensory transduction.

SQ SEQUENCE 1080 AA; 120730 MW; 5950DB968B529401 CRC64;

Query Match 99.8%; Score 5387; DB 10; Length 1080;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 1055; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNWALNNHQEEEEPRRIEISDSLENLKSSDFYQLGGGALNSSEKPKRIDFWRSGLM 60

Db 24 MNWALNNHQEEEEPRRIEISDSLENLKSSDFYQLGGGALNSSEKPKRIDFWRSGLM 83

QY 61 GFAMQOQOQLOHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFSS 120

Db 84 GFAMQOQOQLOHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFSS 143

QY 121 GIYQWDDANKIRREEVLVSMCDQRARMLQDQFSVSNVHVALAILVSTFHYHKNPASID 180

Db 144 GIYQWDDANKIRREEVLVSMCDQRARMLQDQFSVSNVHVALAILVSTFHYHKNPASID 203

QY 181 QETFAEYTARTAFERPLLSGVAYAEKVVNFEREMFERQHNVIKTMDRGEPSVRDEVAP 240

Db 204 QETFAEYTARTAFERPLLSGVAYAEKVVNFEREMFERQHNVIKTMDRGEPSVRDEVAP 263

QY 241 VIFSQDSVSYLESLDMSGEEDRENILRARETGKAVLTSPERLLETHHLGVLTFFPVYKS 300

Db 264 VIFSQDSVSYLESLDMSGEEDRENILRARETGKAVLTSPERLLETHHLGVLTFFPVYKS 323

QY 301 SLPENPTVEERIAAATAGYLGGAFTVESLVENLLGOLAGNQAIVVHVYDITNASDPLVMYG 360

Db 324 SLPENPTVEERIAAATAGYLGGAFTVESLVENLLGOLAGNQAIVVHVYDITNASDPLVMYG 383

QY 361 NQDEEADRSLSHESKLDGDFGDFPRKHKMICRYHQKAPIPLNVLTTPVLPFAIGFLVGYYLY 420

Db 384 NQDEEADRSLSHESKLDGDFGDFPRKHKMICRYHQKAPIPLNVLTTPVLPFAIGFLVGYYLY 443

QY 421 GAAMHIVKVEDDFHEMQELKVRAEAADVAKSQFLATVSHSHEIRTPMNGILGMLAMDTEL 480

Db 444 GAAMHIVKVEDDFHEMQELKVRAEAADVAKSQFLATVSHSHEIRTPMNGILGMLAMDTEL 503

QY 481 SSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540

Db 504 SSTORDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 563

QY 541 RNKGIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600

Db 564 RNKSIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 623

QY 601 EPKNALNGGVSEEMIVWSKQSSYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660

Db 624 EPKNALNGGVSEEMIVWSKQSSYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDISSNV 683

QY 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSTSRNYGGTGIGLSISKCLVELMRGQINF1 720

Db 684 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSTSRNYGGTGIGLSISKCLVELMRGQINF1 743

QY 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKKNVEHL PSTFKGMKAI VVDKPVRAAVTRYH 780

Db 744 SRPHIGSTFWFTAVLEKCDKCSAINHMKKNVEHL PSTFKGMKAI VVDKPVRAAVTRYH 803

QY 781 MKRLGINVDVVTSLKTAVVAAAFAERNGLPTKPKQLDMILVEKDSWISTEDNDSEIRLL 840

Db 804 MKRLGINVDVVTSLKTAVVAAAFAERNGLPTKPKQLDMILVEKDSWISTEDNDSEIRLL 863

QY 841 NSRTNGNVHHKSPKALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELR 900

Db 864 NSRTNGNVHVKSPKALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELR 923
QY 901 KTRQOHPEGSSPATLKSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCVCAESGQVALGL 960
Db 924 KTRQOHPEGSSPATLKSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCVCAESGQVALGL 983
QY 961 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKEAKEKTNLEWHLPILAMTADVIHATYE 1020
Db 984 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKETKEKTNLEWHLPILAMTADVIHATYE 1043
QY 1021 ECLKSGMDGYVSKPFEEENLYKSVAKSFKPNPISPSS 1057
Db 1044 ECLKSGMDGYVSKPFEEENLYKSVAKSFKPNPISPSS 1080

RESULT 5
Q9FRY7 ID Q9FRY7 PRELIMINARY; PRT; 974 AA.
AC Q9FRY7;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Histidine kinase 1.
GN ZMHK1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Golden Cross Bantam T51;
RA Sakakibara H., Sugiyama T.;
RT "Cloning and characterization of maize response regulators.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042270; BAB20583.1; -.
DR HSSP; P06143; 1AB6.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR006189; CHASE.
DR InterPro; IPR003661; His_kinA.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF03924; CHASE; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00512; Hiska; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; Hiska; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50839; CHASE; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 974 AA; 108074 MW; 3EF67B0202D839F0 CRC64;

Query Match 50.1%; Score 2705.5; DB 10; Length 974;
Best Local Similarity 57.9%; Pred. No. 4.4e-168;
Matches 562; Conservative 136; Mismatches 211; Indels 61; Gaps 16;
QY 111 WIIIVGISSGIYQW-----MDDANKIRREEVLVSMCDQARMLQDQFSVNVHVALA 164
Db 22 W-VLTAVVCSAVMHWTLRRDSMD----RAEERLVSMCEERARMLQEQFGVTNVHVAIA 75
QY 165 ILVSTFHYHKNPSAIDQETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIK 224
Db 76 ILISTFNFEKSPPAIDQDTFAKYTARTSFERPLLSGVAFQAQRVFHHEREMFESQQGWVWN 135
QY 225 TMDRGEPSVRDEYAPVIFSQDSVSYLESMDMSGEEDRENILRARETGKAVLTSPFRLL 284

Db 136 TMQR-EPAPPOVEYAPVIFSQDTVSYLARIDMMSGEEDRENIFRARTTGKAVLTNPFRL 194
QY 285 ETHHLGWLTTFPVYKSSLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGNQAIWV 344
Db 195 GSNHLGVLTFAVYRDLPADASVEQORVEATIGYLGAFDVESLVENLLSKLAGNQDIV 254
QY 345 HVYDITNASDPLVMYGNQDEEADRSLSHESKLDPGDPPFRKHMI CRYHQKAPILNVLTT 404
Db 255 NVYDVTNASDAMVLYGFPSSLDQVFLHVSMLDPGDPPFRKHEMRCRYRQKLEMPWSAITN 314
QY 405 VPLFFAIGFLVGYLYGAAMHI VKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTP 464
Db 315 PLGTFVIWMLLGYSIAAAYSRYDKVTEDCRKMBELKTQAEAAADVAKSQFLATASHEIRTP 374
QY 465 MNGILGMLAMLLDTLSSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLEESVPPFD 524
Db 375 MNGVLGMLDMLLTGDTLTMTQKDYAQTAQMCGRALITLINDVLDRAKIEAGKLEAVPFD 434
QY 525 IRSILDDVLSLFEESRNKGIELAVFVSDKVPETIVKGDGRFRQIIINLVGNSVKFTEKG 584
Db 435 LRSLMDDVVSFLSSKSREKCIELAVFVCDNVKVVIGDPWRFRQILTNLVGNVAKFTEG 494
QY 585 HIFVKVHLAEQSKDESEP--KNALNGGVSEEMIVVSKQSSYNTLSGYEAADGRNSWDSFK 642
Db 495 HVFVRVCLAENSNEANQVLHGAMNG--KGRVESTANGAFNTLSGFEEADRRNSWQYFK 552
QY 643 HLVSEEQSL-----SEFDISSNVRLMVSIEDTGIGIPLVAQGRVMPFMQADSSTSR 694
Db 553 LLLSDKESLDDLESENSNQSDSDRVTLAISIEDTGVGIPLQAQDRVTFPMQADSSTSR 612
QY 695 NYGGTGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKKNVEH 754
Db 613 NYGGTGIGLSISKCLAEIMGQISFTSHPSVSGTFTFSATLKHSK-DISGSSRSLSLSEA 671
QY 755 LPSTFKGMKAIIVDAKPVRAAVTRYHMKRLGINVDVVTSLKTA VAAAFERNGSPLPTK 814
Db 672 LPTAFKGMKAILVDGRPVRSVTRYHLKRLGILLQVNNMNAV---KAPFGQNGAAGSR 728
QY 815 PQLDMILVEKDSWISTEDNDSEIRLLN---SR TNGNVHVKSPKALFATNITNSEFDRAK 871
Db 729 EKASILFIESDFW---RPETDVQLNLNHLREQKNGQL-SDGHKVVLVLT-----SEADKDK 779
QY 872 SAGFADTVIMKPLRASMIGACLQQVLEL----RKTRQOHPEGSSPATLKSLLTGKKILV 927
Db 780 YGSIFDIVMCKPIRASTIASSIQQLLKVEIAERKDNQ-----NRPSFLRSLLVGKNILV 834
QY 928 DDNIVNRRVAAGALKKFGAEVVCVCAESGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQ 987
Db 835 DDKNVNLRVAAAALKKYGANVSCVESGKDAISLLQPPPHRFDACFMDVQMPMDGFEATGQ 894
QY 988 IRMMEKEAKEK-----TNLEWHLPILAMTADVIHATYEECLKSGMDGYVSKPFE 1036
Db 895 IRQMELKANEERKNKLASIEGSTTAEYHLPVLAMTADVIQATYEECIKSGMDGYVSKPFD 954
QY 1037 EENLYKSVAK 1046
Db 955 EEQLYQAVSR 964

RESULT 6
Q9C5U2 ID Q9C5U2 PRELIMINARY; PRT; 1176 AA.
AC Q9C5U2;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Histidine kinase.
GN AHK2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

RP	[1]	SEQUENCE FROM N.A.	
RX		MEDLINE=21154803; PubMed=11230578;	
RA		Ueguchi C., Koizumi H., Suzuki T., Mizuno T.;	
RT		"Novel family of sensor histidine kinase genes in Arabidopsis	
RT		thaliana.";	
RL		Plant Cell Physiol. 42:231-235(2001).	
DR		EMBL; AB046869; BAB40774.1; -.	
DR		HSSP; P06143; lAB6.	
DR		InterPro; IPR003594; ATPbind_ATPase.	
DR		InterPro; IPR006189; CHASE.	
DR		InterPro; IPR003661; His_kinA.	
DR		InterPro; IPR005467; His_kinase.	
DR		InterPro; IPR001789; Response_reg.	
DR		Pfam; PF03924; CHASE; 1.	
DR		Pfam; PF02518; HATPase_c; 1.	
DR		Pfam; PF00512; Hiska; 1.	
DR		Pfam; PF00072; response_reg; 1.	
DR		ProDom; PD000039; Response_c; 1.	
DR		SMART; SM00387; HATPase_c; 1.	
DR		SMART; SM00388; Hiska; 1.	
DR		SMART; SM00448; REC; 1.	
DR		PROSITE; PS50839; CHASE; 1.	
DR		PROSITE; PS50109; HIS_KIN; 1.	
DR		PROSITE; PS50110; RESPONSE_REGULATORY; 1.	
KW		Kinase; Phosphorylation; Sensory transduction.	
SQ		SEQUENCE 1176 AA; 131859 MW; AC0019CC612361BC CRC64;	
Query Match 47.2%; Score 2546; DB 10; Length 1176;			
Best Local Similarity 52.6%; Pred. No. 1.6e-157;			
Matches 540; Conservative 156; Mismatches 244; Indels 86; Gaps 18;			
QY	73	HSVAVKMNNDLMGNKKGSTFIOEHRALLPKAL-----ILWIIIV 115	
DB	188	HKIYV-----SHSKARGERKEKVKHLQE--ALAPKKQQRAQTSSRGAGWRKKNILLGIL 240	
QY	116	GTISSGIYQWDDANK---IRREEVLVSMCDQRARMLQDFSVSVNHHVHALILVSTFFHY 172	
DB	241	GGVSFSVM-WFWDTNEEIIIMKRRETLANMCDERARVLQDQENVSLNHHVALSILVSTFFH 299	
QY	173	HKNPSAIDQETFAEYTARTAFERPLLSGVAYAELKVNFEREMFERQHNWVIKTM----- 226	
DB	300	GKIPSAIDQRTFEETYERTNFERPLTSGVAYALKVPHSEREFKEKEHGWAIKKMETEQDT 359	
QY	227	-----DRGEPSVRDEYAPVIFSQDSVSYLESLDMMSGBEDRENILRARETGKAVLTS 279	
DB	360	VVQDCVPENFDPAPIQDEYAPVIFAQETVSHIVSVDMMSGBEDRENILRARASGKVLTS 419	
QY	280	PFRLLETHLGVVLTFFPVYKSSLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGN 339	
DB	420	PFKLLKSNHLGVVLTFAVYDTSLPDPATEEQRVEATIGYLGASYDMPSLVEKLLHQLASK 479	
QY	340	QAIVVHVVDITNASDPLVMYGNQDEEADRSLSHESKLDGDFGPRFKHKMICRYHQKAPIPL 399	
DB	480	QTIADVVDYDTTNTSGLIKWYGS--EIGDISEQHISSLDGDPSPRNHEMHCRFKHKLPIPW 537	
QY	400	NVLTTPVLPFFAIGFLVGILYGAAHIVKVVEDDFHEMQELKVRAEAAADVAKSQFLATVSH 459	
DB	538	TAIPTSILVLVITFLVGILYILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSH 597	
QY	460	EIRTPMNGILGMLALLDTELSQTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELE 519	
DB	598	EIRTPMNGVLGMLKMLMDTDLDAKQMDYQAQTAHSGKDLTSLINEVLDQAKIESGRLELE 657	
QY	520	SVPFDIRSILDDVLSLFSEESRNKGIELAVFVSDKVPRIKVGDSGRFRQIIINLVGNSVK 579	
DB	658	NVPFDMRFLDNVSSLLSGKANKEGIELAVYVSSQVPDVVVGDPSPRFRQIITNLVGNISK 717	
QY	580	FT-EKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQSSYNTLSGYEAAAGNSW 638	
DB	718	FTQERGHIFISVHLADEVK---EPL-TIEDAVLKQRLALGCSEGETVSGFPVAVNAGSW 773	
QY	639	DSFKHLVSEEQSLSEFDDISSNVRLMVSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNYGG 698	

DB	774	KNFKTCYSTESQNSD-----QIKLLVTVEDTGVGIPVDAQGRIFTFFMQADSSISRTYGG 828	
QY	699	TGIGLSISKCLVELMRQINFISRPFHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPST 758	
DB	829	TGIGLSISKRLVELMQGEMGVSEPGIGSTFSFTGVFGKAETNTSITKLER--FDLAIQE 886	
QY	759	FKGMKAIIVDDAKPVRAAVTRYHMKRLGINVDVVTSLKTAVVAATAAFERNGSPLTKPQLD 818	
DB	887	FTGLRALVIDNRNIRAETRYELRRLGISADIVSSLRMACTCCISKLEN-----LA 937	
QY	819	MILVEKDSWISTEDNDSEIRLLNSR-TNGNV-HHKSPKLALFATNITNSEFDRAKSAGFA 876	
DB	938	MILIDKDAW-----NKEEFSVLDELFTRSKVTFTTRVPKIFLLATSATLTERSEMKTGLI 992	
QY	877	DTVIMKPLRASMIGACLQOVLELRKTRQHQHPEGSSPATLKSLLTGKKILVDDNIVNRRV 936	
DB	993	DEVVIKPLRMSVLICCIQETLVNGKKRQPNRQRN--LGHLLREKQILVDDNIVNRRV 1049	
QY	937	AAGALKKFGAEVVCESQVALGLLIQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKEAK 996	
DB	1050	AEGALKKYGAIVTCVESGKAALAMLKPPHNFDAFCFMDLQMPMDGFEATRVRRELEREIN 1109	
QY	997	EKTN-----LEWHLPILAMTADVIHATYEELCKSGMDGYVSKPFEENLYKSV 1044	
DB	1110	KKIASGEVSAEMFCFSSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEELVYTAV 1169	
QY	1045	AKSFKP 1050	
DB	1170	ARFFEP 1175	
RESULT 7			
QYFKH3			
ID	Q9FKH3	PRELIMINARY; PRT; 1173 AA.	
AC	Q9FKH3;		
DT	01-MAR-2001	(TremBLrel. 16, Created)	
DT	01-MAR-2001	(TremBLrel. 16, Last sequence update)	
DT	01-MAR-2003	(TremBLrel. 23, Last annotation update)	
DE	Histidine kinase-like protein.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Columbia;		
RX	MEDLINE=98344145; PubMed=9679202;		
RA	Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,		
RA	Tabata S.;		
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence		
RT	features of the regions of 1,381,565 bp covered by twenty one		
RT	physically assigned p1 and TAC clones.";		
RL	DNA Res. 5:131-145(1998).		
DR	EMBL; AB011485; BAB09274.1; -.		
DR	HSSP; P06143; lAB6.		
DR	InterPro; IPR003594; ATPbind_ATPase.		
DR	InterPro; IPR004358; Bact_sens_pr_c.		
DR	InterPro; IPR006189; CHASE.		
DR	InterPro; IPR003661; His_kinA.		
DR	InterPro; IPR005467; His_kinase.		
DR	InterPro; IPR001789; Response_reg.		
DR	Pfam; PF03924; CHASE; 1.		
DR	Pfam; PF02518; HATPase_c; 1.		
DR	Pfam; PF00512; Hiska; 1.		
DR	Pfam; PF00072; response_reg; 1.		
DR	PRINTS; PR00344; BCTRLSENSOR.		
DR	ProDom; PD000039; Response_reg; 1.		
DR	SMART; SM00387; HATPase_c; 1.		
DR	SMART; SM00388; Hiska; 1.		
DR	SMART; SM00448; REC; 1.		
DR	PROSITE; PS50839; CHASE; 1.		

Db 223 HKDDYDLEALEPSPVQEEYAPVIFAQDTVSHVVSLDMLSGKEDRENVLRARSSGKGVLT 282

QY 280 PFRLETHLGVVLTTPPVYKSSLPENPTVEERIAATAGYLGGAFDVESLVENLLQLAGN 339

Db 283 PFPLIKTNRLGVILTFVYKRDLPNSATPERIEATNGYLGGVFDIESLVENLLQQLASK 342

QY 340 QAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDGDPDFRKHKMICRYHQAPIPL 399

Db 343 QTILNVVYDITNHSQPISMYGT-NVSAD-GLERVSPLIFGDPRLRKHMRRCFRKQKPPWPV 400

QY 400 NVLTTVPLFFAIGFLVGYILYGAAMHIVKVEDDDFHEMQELKVRAEAAADVAKSQFLATVSH 459

Db 401 LSMVTSFGILVIALLVAHIIHATVSRHKVEEDCDKMQLKKKAEAAADVAKSQFLATVSH 460

QY 460 EIRTPMNGILGMLAMLDDTELSSQTDYAQTAQVCGKALIALINEVLDRAKIEAGKLELE 519

Db 461 EIRTPMNGVLGMLHMLMDTDLVTQDDYVRTAQASGKALVSLINEVLDOAKIESGKLELE 520

QY 520 SVPFDIRSILDDVLSLSEESRNKGIELAVFVSDKVPEIVKGDGSRFRQIILNVGNSVK 579

Db 521 EVRFDLRGILDDVLSLFSKSKSQKGVELAVISDRVPDMLIGDPGRFQILTNMGNSIK 580

QY 580 FTEKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWD 639

Db 581 FTEKGHIFVTVHLVDELFESEDGETA-----SSPESTLSGLPVADRQRSWE 626

QY 640 SFKHLVSEEQSLSEFDIS-SNVRLMVSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNYGG 698

Db 627 NFKAFFSSNGH--RSFEPSPPDINLIVSVEDTGVGIPVEAQSRIFTTPMQVGPSISRTHGG 684

QY 699 TGIGLSISKLVELMRGQINFISRPHGISTPFWFTAVLEKCDKCSAINHM-----KKPNVE 753

Db 685 TGIGLSISKLVGLMKGEIGFSSTPKVGSFTFTAVFS-----NGMQPAERKNDNNQ 736

QY 754 HLPSTFKGMKAIVVDKPVRAAVTRYHMKRLGINVDVVTSLKTAVVAAAFERNGSPLPT 813

Db 737 PIFSEFRGMKAVVVDHRPARAKVSWYHFQRLGIRVEVVRVEQAL----HYLKIGT--- 788

QY 814 KPQLDMILVEKDSWISTEDNDSEIRLINSRTNGNVHKS PKLALFATNITNSEFDRAKSA 873

Db 789 -TTVNMLIEQBIW--NREADDFIKKLQK----DPLFLSPKILLANSVESSISEALCTG 841

QY 874 GFADTVIMKPLRASMIGACLOQVLELRKTRQOHPEGSSPATLKSLLTGKKILVVDNIVN 933

Db 842 IDPPIVIVKPLRASMLAATLQRLGIGIREPPQHKGPALILRNLLGRKILIVDDNNVN 901

QY 934 RRVAGALKFGEAEVVCAESGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQIRMMEK 993

Db 902 LRVAAGALKKYGADVVCAESGIKAISLLKPPHEFDACFMDIQMPENDGFEATRIRDMEE 961

QY 994 EAKEK-----TNLEWHLPILAMTADVIHATYEECLKSGMDGYVSKPFEENLY 1041

Db 962 EMNKRIKNGBALIVENGKNTSWHLPLVLAMTADVIQATHEECLKCGMDGYVSKPFEAEQLY 1021

QY 1042 KSAKSFKNPISPS 1056

Db 1022 REVSRRFN----SPS 1032

RESULT 9

Q8L816

ID Q8L816 PRELIMINARY; PRT; 1041 AA.

AC Q8L816;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Cytokinin receptor.

GN CKR1.

OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;

OC Catharanthus.

OX NCBI_TaxID=4058;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22166729; PubMed=1217139;

RA Papon N., Clastre M., Andreu F., Gantet P., Rideau M., Creche J.;

RT "Expression analysis in plant and cell suspensions of CrCKR1, a cDNA encoding a histidine kinase receptor homologue in Catharanthus roseus (L.) G. Don.";

RL J. Exp. Bot. 53:1989-1990 (2002).

DR EMBL; AY092025; AAM14700.1; --

DR InterPro; IPR03594; ATPbind ATPase.

DR InterPro; IPR04358; Bact_sens_pr_C.

DR InterPro; IPR06189; CHASE.

DR InterPro; IPR03661; His_kinA.

DR InterPro; IPR05467; His_kinase.

DR InterPro; IPR01789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR PRINTS; PR00344; BCTRLSENSOR.

DR ProDom; PD00039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW Phosphorylation; Receptor; Sensory transduction.

SQ SEQUENCE 1041 AA; 116697 MW; 8A56658493C31C48 CRC64;

Query Match 45.1%; Score 2431.5; DB 10; Length 1041;

Best Local Similarity 50.7%; Pred. No. 4.1e-150;

Matches 522; Conservative 165; Mismatches 248; Indels 95; Gaps 18;

QY 66 QQQQLQHSVAVKMNNNNDLGNKKGSTFIQEHRRALLPKALILWIIIVG-FISSGIYQ 124

Db 59 QQPQLLQHFHQQQIQNTSRS-----TGKWW-----KTLVVVFLAGIFGSMWLFW 103

QY 125 WMDDANKIRREEVLVSMCDQBARMLQDQFSVSNVHVHALAILVSTFHYHKNPSSAIDQETF 184

Db 104 YLSEDSKLRKKETLASCMDERARMLOQDNVSLNVHVALAILVSTFYHGKEPWARDQOTF 163

QY 185 AEYTARTAPERLLSGVAVAKVNVFEREMFERQHNWIKTMD-----RGEF 231

Db 164 EDYTEKTAFERPLTSGVAYALRVLHSEREKFEKQQQWIRKMDTEVQTLGQDLVPEKLEP 223

QY 232 SPVRDEYAPVIFSQDSVSYLESIDMMSGEEDRENILRAETGKAVLTSPFRLLETHLGV 291

Db 224 APVQTEYAPVIFAQKTVSHIVSIDMMSGKEDRENILRARASGKGLTSPFKLLKSNHLGV 283

QY 292 VLTFPVYKSSLPENPTVEERIAAATAGYLGAFDVESLVENLLQLAGNQAIVVHVYDITN 351

Db 284 VLTFAVYNTDLPPEATREQRINATVGILGASYDVPSPSLVEKLLHQASKQTIANVYDITD 343

QY 352 ASDPLVMYGNQDEEADRSLSHESKLDGDPDFRKHKMICRYHQKAPIPLNVLTTPVLPFFAI 411

Db 344 KSAPIKMYG--DAANDTGLPRISQLDGDPSPRKHEMHCRFKQKPPPTWTAIIASVGVLVI 401

QY 412 GFLVGYILYGAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGM 471

Db 402 TLLLGHIFFHAAINRIAKVERDYREMMALKHRAEAAIAKSOFLATVSHEIRTPMVGVLGM 461

QY 472 LAMLLDTELSSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDD 531

Db 462 LQMLMGNTLDVKQLDYAETAHASGKDLISLINEVLDOAKIESGRLELEAVPFOLRADLDK 521

QY 532 VLSLFSEESRNKGIELAVFVSDKVPEIVKGDGSRFRQIILNVGNSVKFT-EKGHIFVKV 590

Db 522 VVSLLSGKSHEKDIELAVYVSDQVPEVIGDPGRFRQITNLVGNISIKFTKDKGHIFVSV 581

QY 591 HLAEQSKDESEPKNALNGGVSEEMIVWSKQS--SYNTLSGYEAAADGRNSWDSFKHL--VS 646

Db 582 HLADEVKSPLDIKDEV---LKQSLTLIQDRSTASFNTLSGFPVVDWRWSWEKFNLSGMP 638

QY 647 EEOQLSEFDDISSNVRMLMVSIEDTGTGIGIPLVAQGRVFMFPMQADSSTSRNYGGTGIGLSIS 706

Db 639 EE-----SKIKLLVTVEDTGDGIVYDAQDRIFTFPVQADSSTSRKYGGTGIGLSIS 690

QY 707 KCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLRSTFKGMKAIV 766

Db 691 KRLVDLVGGEIGFVSEPGTGSTFSPTAAFTKAETITGIT--KWEQYDLAVSEFRELKALV 748

QY 767 VDAKPVRAAVTRYHMKRLGINVDVVTSLKTAV-----VAAAFAFERNGSPLPTKPLQDMI 820

Db 749 VDEKSIRAEVTRYQLKRLVSVSDIASTVEAAYSHLSADVNSSASER-----VSMV 798

QY 821 LVEKDSWISTEDNDSEIRLLN-----SRTNGNVHHKSPKLALFATNITNSEFDRAK 871

Db 799 LIDEDSW----DNEIMARYVGCLKKSDQTASRPSMGM---NPKIFLLANPKSFSDCIELK 851

QY 872 SAGFADTVIMKPLRASMIGACLQQVLELRKTRQOHPEGSSPATLKSLLTGKKILVVDDNI 931

Db 852 STGLVDNVLTKPLRLSILISCLIGESIGFGRTRQ--VTRSNPSTIGNLLKGRMLVVDDNP 909

QY 932 VNRVVAAGALKKFGAEVVCESGQVALGLLIQIPHTFDACFMDIQMPQMDGFEATRQIRMM 991

Db 910 VNRKVAELALRKYGAVVTCEASGEAALQRLKPPHDFACFMDLQMPENDGFEATQKIRHL 969

QY 992 EKEAKEKT-----NLEWHLPILAMTADVIAHYEELCKSGMDGYVSKPFEEN 1039

Db 970 EREYNENVKSIGEIGTDKSDTEAYWHTPILAMTADLIQATNEKCRKCGMDGYVSKPFDDEQ 1029

QY 1040 LYKSVAKSFK 1049

Db 1030 LYSAVAPFFK 1039

RESULT 10

Q9FZK3

ID Q9FZK3 PRELIMINARY; PRT; 1092 AA.

AC Q9FZK3;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE F17L21.11.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,

RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,

RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,

RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,

RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,

RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,

RA Ecker J.R.;

RT "Genomic sequence for Arabidopsis thaliana BAC F17L21 from chromosome

RT I.;"

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RA Ecker J.R.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,

RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,

RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,

RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,

RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,

RA Theologis A., Ecker J.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC004557; AAF99730.1; -

DR InterPro; IPR003594; ATPbind ATPase.

DR InterPro; IPR004358; Bact_sens_pr_C.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR PRINTS; PR00344; BCTRLSENSOR.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 2.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW Phosphorylation; Sensory transduction.

SQ SEQUENCE 1092 AA; 122824 MW; 72530C55873A216B CRC64;

Query Match 44.5%; Score 2402; DB 10; Length 1092;

Best Local Similarity 48.0%; Pred.No.3.8e-148;

Matches 528; Conservative 162; Mismatches 257; Indels 154; Gaps 20;

QY 1 MNWALNNHQEEEEPRRIEISDSELENLKSSDFYQLGGGALNSSEKPKRIDFWR---- 56

Db 25 VSWFVDNGIEDKS--GLLVGSVGDLEKTK-----MTTLKKKKMKWFWFNKISS 69

QY 57 SGLM--GFAKMQQQQLQHSVAVKMNNNNNNDLMGNKKGSTFQIEHRALLPKALILWIII 114

Db 70 SGLKIPSFs-----YQFLGSVKFN-----KAWRKLVVVVVVF 102

QY 115 VGFISGIYQWMDANKIRREEVLVSMCDQARMLOQFVSVNHVHALAILVSTFHYHK 174

Db 103 WVLVSIWTFWYFSSQAMEKRKETLASMCDERARMLOQFNVSMNVHVAQMSILISTFHGK 162

QY 175 NPSAIDQETFAEYTAARTAFERPLLSGVAYAEKVNVFEREMFERQHNVVTKM----- 226

Db 163 IPSAIDQRTFSEYTDRTSFERPLTSGVAYAMRVLHSEEREFEERQOQWTIRKMSLEQNPV 222

QY 227 -----DRGEPSVRDEYAPVIFSQDSVSYLESLDMMSGEEDRENILRARETGKAVLTS 279

Db 223 HKDDYDLEALEPSPVQEEYAPVIFAQDTVSHWVSLDMLSGKEDRENVLARSSSGKGLTA 282

QY 280 PFRLETHHLGVVLTFFPVYKSSLPENPTVEERIAATAGYLGGAFFVESLVENLLGOLAGN 339

Db 283 PFPLIKTNRLGVILTFAVYKRDLPNATPKERIEATNGYLGGVDFIESLVENLLQOLASK 342

QY 340 QAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDGDFDPFKHKM----- 387

Db 343 QTILVNVDITNHSQIPSMYGT-NVSAD-GLERSVPLIFGDPLRKHEMRCRYQLAHTYV 400

QY 388 -----ICRYHQKAPIPLNVLTTVPLFFAIGFLVGYILYGAAMHIV 427

Db 401 CNFFLFARIQVLTFCCELLPLCRFKQKPPWPVLSMVTSGILVLTALLVAHIIHATVSRIH 460

QY 428 KVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTELSSTQDXY 487

Db 461 KVEEDCDKMKQLKKKAEAADVAKSQFLATVSHSIRTPMNGVLGMLHMLMDTELDVTQQDY 520

QY 488 AQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSFSEESRNKGIEL 547

Db 521 VRTAQASGKALVSLINEVLDQAKIESGKLEEEVRFDLRGILDVLSFSSKSKQKGVEL 580

QY 548 AVFVSDKVPKIEVKGDSGRFRQIIINLVGNSVKTEKGHIFVKVHLAEQKDESEPKNALN 607

Db 581 AVYISDRVPDMLIGDPGRFRQILTNLMGNSIKTEKGHIFVTVHLVDELFSIDGETA-- 638

QY 608 GGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSPKHLVSEEQSLSEFDIS-SNVRLMVS 666

Db 639 -----SSPESTLSGLPVADRQRSWENPKAFSSNGH--RSFEPSPPDINLIVSV 684

QY 667 EDTGIGIPLVAQGRVPMFMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFISRPHIG 726

Db 685 EDTGVGIPVEAQSRIFTPFMQVGPSISRTHGGTGIGLSISKCLVGLMKGEIGFSSTPKVG 744

QY 727 STFWFTAVLEKCDKCSAINHM-----KKPNVEHLPTFKGMKAIIVVDKPVRAAVTRYHM 781

Db 745 STFTFTAVFS-----NGMQPAERKNDNNQPIFSEFRGMKAVVVDHRRAPAKVSWYHF 796

QY 782 KRLGINVDVVTSLKTAVVAAAFAERNGSPLPKQQLDMILVEKDSWISTEDNDSEIRLLN 841

Db 797 ORLGIRVEVVRVEQAL-----HYLKIGT-----TTVNMILIEQEIW--NREADDFIKKLQ 845

QY 842 SRINGNVHVKSPKALPATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELRK 901

Db 846 K----DPLFLSPKLILLANSVSESSSEALCTGIDPPVIVKPLRASMLAATLQRLGIGI 901

QY 902 TRQHQPEGSSPATLKSLLTGKKILVDDNIIVNRRVAAGALKKFGAEVVCAESGQVALGLL 961

Db 902 REPPQHKGPALILRNLLGRKILIVDDNNVLRVAAGALKKYGADVVCAESGIGKAISLL 961

QY 962 QIPHTFDACFMDIQMPQMDGFEATRQIRMMEXBAKEK-----TNLEWHLPILA 1009

Db 962 KPPHEFDACFMDIQMPMDGFEATRIRDMEEHMKRIKNGEALIVENGKNTSWHLPLVA 1021

QY 1010 MTADVIHATYEECLKSGMDGY 1030

Db 1022 MTADVIQATHEECLKCGMDGY 1042

RESULT 11

Q8RYG4 ID Q8RYG4 PRELIMINARY; PRT; 1023 AA.

AC Q8RYG4;

DT 01-JUN-2002 (TReMBLrel. 21, Created)

DT 01-JUN-2002 (TReMBLrel. 21, last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, last annotation update)

DE Putative histidine kinase.

GN P0592G05.13.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, PAC

RT clone:P0592G05.";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AP004672; BAB90827.1; --

DR Gramene; Q8RYG4; --

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kinA.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.

KW Kinase; Phosphorylation; Sensory transduction.

SQ SEQUENCE 1023 AA; 113219 MW; 469AC35146CDF62B CRC64;

Query Match 44.0%; Score 2375; DB 10; Length 1023;

Best local Similarity 51.6%; Pred.No. 2e-146;

Matches 508; Conservative 154; Mismatches 229; Indels 94; Gaps 21;

QY 108 LILWIIIVGFISSGIYQWMDANKIRREEVLSVSMCDQARMQLQDQFSVSNVHVALAILV 167

Db 84 LLLWILAGSLGSFYLFLEFMAQSLDKRDSLASMCDERARMQLQDQFNVSMNHLQALAILV 143

QY 168 STFHYHKNPISAIDQETFAEYRTARTAFERPLLSGVAYAEKVNFEREMFERQHNWVIKTM- 226

Db 144 STFHSKTPSAIDQMTFARYAERTAFERPLTSGVAYAVRVTHGEREQFERQQGWAIKMY 203

QY 227 -----DRGEPSP-----VR---DEYAPVIFSQDSVSYLESLDMMSGEEDRENILRA 269

Db 204 SSSNKKQSGPGPGDAAVAEIREPAEYAPVIFAQDAYKHVTSFDMLSGNEEDRONILRA 263

QY 270 RETGKAVLTSPPRLLETHLGVVLTFFPVYKSSLPENPTVEERIAATAGYLGAFDVESLV 329

Db 264 RKSGKGLTAPFKLL--NNRLGVILTYVYKELPAYARPHERIAQAIGYLGIFDIQALV 322

QY 330 ENLLGQLAGNQAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDGDPFRKHKMIC 389

Db 323 EKLKQLASQESIMVNVYDTNES-PISMYG---DDTSGMCHSVLVNFGDPSRKHEMHC 378

QY 390 RYHQKAPIPLNVLTTPVPLFFAIGFLVGYILYGAAMHIVKVEDDFHEMQELKVRAEADVA 449

Db 379 RFEKKPPWPWLAITSSFGTLVIALLTGHIFOATVHRIAKVEDDFHKMSELKKRAEDADVA 438

QY 450 KSQFLATVSHSIRTPMNGILGMLAMLDDTELSSTORDYAQTAQVCGKALIALINEVLDR 509

Db 439 RSQFLATVSHSIRTPMNGVLGMLQMLMDTDLDTTQQDYVRTAQASGKALVSLINEVLDR 498

QY 510 KIEAGKLELESVPFDIRSILDDVLSFSEESRNKGIELAVFVSDKVPKIEVKGDSGRFRQI 569

Db 499 KIESGKLELETVPFDLRTVCDDILSLFCGKAQEKGLELAVVSDQVPQILIGDPGRIRQI 558

QY 570 IINLVGNSVKFTEKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQSSYNTLSGY 629

Db 559 ITNLVGNSTKFTERGHILYTVHVVEEVMSCLEVETGI-----QNTNTLSGY 604

QY 630 EAADGRNSWDSF---KHLVSEEQSLSEFDISNVRLMVSIEDTGIGIPLVAQGRVMPF 685

Db 605 PVANRRCSWESIRLFNRELHSSSEKSFAP-ASDSISLVISVEDTGVGIPFEAQSRVTFPF 663

QY 686 MQADSTSRNYGGTGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAIN 745

Db 664 MQVGPSIARIHGGTGIGLSISKCLVGLMKGEIGFASKPHVSGSTFTTAVLMRA----- 716

QY 746 HMKKPNVEHLPSTFKGMKAIIVDAKPVRAAAVTRYHMKRLGINVDVVTSLKTAVVAAAFA 805

Db 717 HCKGNDIK--SSEFKGINALVVDHRPVRKAVTKYHLQRLGVKTELTAELNQFI-----SK 769

QY 806 RNSGSLTAK---LVLIDKETWL---KESCHTPLLNVNKLNNDKPDSPKLFLLGSSASS 821

Db 865 SEFDRAKSAGFADT-----VIMKPLRASMIGACLQQVL-ELRKTR-QQHPEGSSPATL 915

Db 822 PK-----GGSDTSREHNLNVIMKPLRASMLQVSLRRALGGVDKVCNMGVNGNS--TL 872

QY 916 KSLLTGKKILVDDNIIVNRRVAAGALKKFGAEVVCAESGQVALGLLQIPHTFDACFMDIQ 975

Db 873 G S L L H K K Q I I V V D N I V N L K V A A G A L K K Y G A E V T C A D S G K K A I T L L K P H N F D A C F M D I Q 932

QY 976 M P Q M D G F E A T R Q I R N M M E K E A K E K T N ----- L E W H L P I L A M T A D V I H A T Y E E C L K 1024

Db 933 M P E M D G F E A T R R I R V N E R D L N E R I E R G E A P P E C A S I Q R W R T P I L A M T A D V I Q A T H E E C L K 992

QY 1025 S G M D G Y V S K P F E E N L Y K S V A K S F K 1049

Db 993 S E M D G Y V S K P F E G E Q L Y S E V A R F F Q 1017

RESULT 12

Q8S6P5 PRELIMINARY; PRT; 925 AA.

AC Q8S6P5;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Putative histidine kinase.

GN OSJNBA0073L01.1.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,

RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,

RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,

RA Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,

RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;

RT "Oryza sativa chromosome 10 BAC OSJNBA0073L01 genomic sequence.";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC092548; AAM18726.1; -.

DR Gramene; Q8S6P5; -.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR006189; CHASE.

DR InterPro; IPR003661; His_kina.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF03924; CHASE; 1.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; Hiska; 1.

DR Pfam; PF00072; response_reg; 1.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; Hiska; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS50839; CHASE; 1.

DR PROSITE; PS50109; HIS_KIN; 1.

DR PROSITE; PS50110; RESPONSE_REGULATORY; 2.

KW Kinase; Phosphorylation; Sensory transduction.

SQ SEQUENCE 925 AA; 102928 MW; 6046D9AC28824219 CRC64;

Query Match 41.7%; Score 2248.5; DB 10; Length 925;

Best Local Similarity 52.4%; Pred. No. 3.2e-138;

Matches 495; Conservative 144; Mismatches 223; Indels 83; Gaps 20;

QY 133 R R E E V L V S M C D Q A R M L Q D Q F S V S V N H V H A L I I V S T F H Y H K N P S A I D Q E T P A E Y T A R T A 192

Db 8 R R I E N L E N M C D E R A R M L Q D Q F N V S M N H V H A L I I V S T F H G K N P S A I D Q K T F E D F T A R T T 67

QY 193 F E R P L L S G V A Y A E K V V N F E R M F E R Q H N W V I K M ----- D R G E F S P V R D E Y A 239

Db 68 F E R P L M S G V A Y A L K V L H S E R E L F E Q L G W K I K M E T E D Q S L V H D Y N P E K L Q P S P V Q D E Y A 127

QY 240 P V I F S Q D S V S Y L E S L D M S G E E D R E N I L R A R E T G K A V L T S P F R L L E T H L G V V L T F P V Y K 299

Db 128 P V I F S Q E T V K H I I S V D M S G K E D R D N I L R S R A T G K A L T A P F P L L K S N H L G V V L T F T V Y K 187

QY 300 S S L P E N P T V E E R I A A T A G Y L G G A F D V E S I V E N L L G Q L A G N O A I V V H V D I T N A S D P L V M Y 359

Db 188 Y D L P P D A T P E E R I E A T G Y L G A S F D V P S L V E R L L E Q L A S K Q I V V R L Y D I T N H T Y P T K M Y 247

QY 360 G N Q D E E A D R S L S H E S K L D F G D P P F R K H M I C R Y H Q K A P I P L N V L T T V P L F F A I G L V G Y I L 419

Db 248 - D S D V I A S D D L - H I S N I D F G D P T R K H V M H C R F K H A P S L P W S A I M I S S A V A I I V L V G Y I I 305

QY 420 Y G A A M H I V K V E D D F H E M O E L K V R A E A A D V A K S Q F L A T V S H E I R T P M N G I L G M L A M L L D T E 479

Db 306 Y A T L N S L E A E A D N Y T T M R D L K G R A E A A D V A K S Q F L A T V S H E I R T P M N G V L G M L Q M L M D T E 365

QY 480 L S S T Q R D Y A Q T A Q V C G K A L I A L I N E V L D R A K I E A G K L E S V P F D I R S I L D D V L S L F S E E 539

Db 366 L D T T Q R D F V V T A Q E S G K S L I N L I N E V L D L A K I E S G K I E L E A V R F D V R D I L D N V S L F S E K 425

QY 540 S R N K G I E L A V F V S D K V P E I V K G D S G R P F Q I I I N L V G N S V K F T E K G H I F V K V H L A E Q S K - - 597

Db 426 S W A K G I E L A V L V S D Q V P D V L I G D P W R F R Q I I T N L V G N S M K F T E Q G H I F I R V H L I E E V K R K 485

QY 598 - - - D E S E P K N A L G V S E E M I V V S K Q S - S Y N T L S G Y E A A D G R N S W D S F K H L V S E E Q S L S 652

Db 486 M E A L D D T S P E N I - - - - - E V T A N S K N T M P Y N T L S G L E V A N N R K T L E S F R - - M F K D S S - - 534

QY 653 E F D I S S N V R L M V S I E D T G I G I P L V A Q G R V F M P F M Q A D S S T S R N Y G G T G I G L S I S K C L V E L 712

Db 535 - - D A I D S V N L L V T V E D T G I G I T K D A Q T R I F T P F M Q A D G S T S R Y G G T G I G L S I T K R L V E L 592

QY 713 M R G Q I N F I S R P H I G S T F W T A V L E K D C K S A I N H M K K P N V E H L S T F K G M K A I V V D A K P V 772

Db 593 M G E I G F V S K P G V S S T F S T A I F K E N R K D P - - G D I K R Y C P E P T P D F Q G M R A L V V D G R C A 650

QY 773 R A A V T R Y H M K R L G I N V D V V T S L K T A V V A A A A F E R N G S P L P T K P Q L D M I L V E K D S W I S T E D 832

Db 651 R A E V T M V H L R L I G I Q C D L A A T S E S A L - - S A L L E S C N S S V - - K S S L N M V L V D K E A W - - - - G 702

QY 833 N D S E I R - - - - L L N S R T N G N V H - - H K S P K L A L F A T N I T N S E F D R A K S A G F A D T V I M K P L R A 886

Db 703 E D S G L A F F R C L I D L R L K G T L K S W Q T M P K F F L L A G S I T P A D S D C L R L A G Y S N S - I R K P I R L 761

QY 887 S M I G A C L Q Q V L E L R K T R Q Q H P E G S S P A T L K S L L T G K K I L V D D N I V N R R V A A G A L K K F G A 946

Db 762 S T V A A C L S K A L G V G L T G R R S R D N S - - L V L R S V L T G K N I L V D D N A V N R I V A A G A L K K Y G A 819

QY 947 E V V C A E S G Q V A L G L L Q I P H T F D A C F M D I Q M P Q M D G F E A T R Q I R N M M E K E A K E K T N L E W H L P 1006

Db 820 I V T C V D S G K E A I S R L Q P P H K F D A C F M D V Q M P E M D G F E A T R L V R S V E - - - - S K I N - - - - - 869

QY 1007 I L A M T A D V I H A T Y E E C L K S G M D G Y V S K P F E E N L Y K S V A K S F K P N 1051

Db 870 - - - - - D T I Q A - - - - - - - - - - - - A S A K N P F G D N N I A K Q - - K S Y A V N 895

RESULT 13

Q8GUG0

ID Q8GUG0 PRELIMINARY; PRT; 652 AA.

AC Q8GUG0;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Histidine kinase-like protein.

GN AT5G35750.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,

RA Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,

RA Deng J.M., Hayashizaki Y., Hsuan V.W., Lee J.M., Ishida J., Kamiya A.,

RA Kawai J., Kim C.J., Narusaka M., Onodera C.S., Quach H.L., Sakurai T.,

RA Satou M., Seki M., Shinn P., Tang C.C., Toroumi M., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J., Theologis A.,
RA Davis R.W.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT002530; AAO00890.1; -.
KW Kinase.
SQ SEQUENCE 652 AA; 72656 MW; 705751BAA15C4E05 CRC64;

Query Match 31.5%; Score 1698.5; DB 10; Length 652;
Best Local Similarity 52.9%; Pred. No. 1.7e-102;
Matches 359; Conservative 106; Mismatches 171; Indels 43; Gaps 11;

Qy 387 MICRYHQKAPIPLNVLTTVPLFFAIGFLVGYILYGAAMHIVKVEDDFHEMQELKVRAEA 446
Db 1 MHCRFKHLPPIPTAITPSILVLVITFLVGYILYEAIRNIAIVVEDCQKMRELKARAEA 60

Qy 447 DVAKSQFLATVSHEIRTPMNGILGMLAMDTELSSQTDYAQTAQVCGKALIALINEVL 506
Db 61 DIAKSQFLATVSHEIRTPMNGVLGMLKMLMDTDLDAQMDYAQTAHSGKDLTSLINEVL 120

Qy 507 DRAKIEACKLELESVPFDIRSILDDVLSLFSEESRNKGIELAVFVSDKVPEIVKGDGRF 566
Db 121 DQAKIESGRLELENVPFDMRFILDNVSSLLSGKANKEGIELAVVSSQVPDVVGDPSRF 180

Qy 567 RQIIINLVGNSVKFT-EKGHIFVKVHLAEQSKDESEPKNALNGVSEEMIVVSKQSSVNT 625
Db 181 RQIIINLVGNSIKFTQERGHIFISVHLADEVK---EPL-TTEDAVLKQRLALGCSSEGET 236

Qy 626 LSGYEAADGRNSWDSFKHLVSEEQSLSEFDDISSNVRLMVSIEDTGIGIPLVAQGRVFMFP 685
Db 237 VSGFPAVNAWGSWKNFKTCYSTESQNSD-----QIKLLVTVEDTGVGIPVDAQGRIFTPF 291

Qy 686 MQADSSSRNYGGTGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAIN 745
Db 292 MQADSSSRNYGGTGIGLSISKRLVELMQEMGFVSEPGIGSTFSFTGVFGKAETNTSIT 351

Qy 746 HMKKPNVEHLPSTFKGMKAIVVDKPVRAAAVTRYHMKRLGINVDVVTSLKTAVVAAAPE 805
Db 352 KLER--FDLAIQEFTGLRALVIDNRNIRAEVTRYELRRLGISADIVSSLRMACTCCISKL 409

Qy 806 RNGSPLPKPOLDMILVEKDSWISTEDNDSEIRLLNSR-TNGNV-HHKSPKLALFATNIT 863
Db 410 EN-----LAMILIDKDAW-----NKEEFSVLDELFTRSKVTFTRPVKIFLLATSAT 455

Qy 864 NSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELRKTRQHPGEGSSPATLKSLLTGKK 923
Db 456 LTERSEMKSTGLIDEVWIKPLRMSVLICLQETLVNGKKRQPNRQRN---LGHLLEKQ 512

Qy 924 ILVDDNIVNRRVAAGALKKFGAEVVCASGQVALGLLQIPHTEFACFMDIQMPQMDGFE 983
Db 513 ILVDDNLVNRVAEGALKKYGAIVTCVESGKAALAMLKPPHNFEDACFMDLQMPMDGFE 572

Qy 984 ATRQIRMEKEAKEKTN-----LEWHLPIAMTADVIHATYEECLKSGMDGYV 1031
Db 573 ATRRVRELBREINKIASGEVSAEMFCFSSWHVPILAMTADVIQATHEECMKCGMDGYV 632

Qy 1032 SKPFEENLYKSVAKSFKP 1050
Db 633 SKPFEVEVLYTAVRFFEP 651

RESULT 14
Q9AUQ0 PRELIMINARY; PRT; 627 AA.
AC Q9AUQ0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Histidine-kinase like protein.
GN OSJNBA005819.1.
OS Oryza sativa (Rice).
OC Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., King L., Kirchoff K.A., de la Bastide M., Preston R.R.,
RA Nascimento L.U., Vil M.D., Baker J.P., Miller B., Cunniss D.M.,
RA Kuit K.H., Rodriguez S., Santos L., Zutavern T., Balijs V.S.,
RA Shah R.S., Bahret A., Bal H.P., O'Shaughnessy A., Dedhia N.N.,
RA McCombie W.R.;
RT "Genomic Sequence For Oryza sativa, Nipponbare Strain, Chromosome X,
RT Clone OSJNBA005819, Complete Sequence."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC083945; AAK13126.1; -.
DR Gramene; Q9AUQ0; -.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF00072; response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 2.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 627 AA; 68569 MW; CAB234F47595D7CD CRC64;

Query Match 19.3%; Score 1042; DB 10; Length 627;
Best Local Similarity 45.3%; Pred. No. 1.4e-59;
Matches 240; Conservative 90; Mismatches 140; Indels 60; Gaps 16;

Qy 547 LAVFVSDKVPEIVKGDGRFRQIILNLVGNVSVKFTKGHIFVKVHLAEQSK-----DES 600
Db 1 MAVLVSDQVPDVLIGDPWRFRQIITNLVGNMVKFTEQGHIFIRVHLIEEVKRMALDDT 60

Qy 601 BPKNALNGVSEEMIVVSKQS-SYNTLSGYEAADGRNSWDSFKHLVSEEQSLSEFDDISSN 659
Db 61 SPENI-----EVTANSKNTMPYNTLSGLEVANNRKTLESFR--MFKDSS-----DAIDS 107

Qy 660 VRLMVSIEDTGIGIPLVAQGRVFMFPQADSSSTRNYGGTGIGLSISKCLVELMRGQINF 719
Db 108 VNLLVTVEDTGIGITKDAQTRIFTPFMQADGSTSRTYGGTGIGLSITKRLVELMGGEIGF 167

Qy 720 ISRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPSTFKGMKAIVVDKPVRAAVTRY 779
Db 168 VSKPGVSTFSFTAIFKENRKDP--GDIKRYCPEPTPDFQGMRALVVDGRCARAEVTMY 225

Qy 780 HMKRLGINVDVVTSLKTAVVAAAFAERNGSPLTPKPOLDMILVEKDSWISTEDNDSEIR- 838
Db 226 HURRLGIQCDLAATSESAL--SALLESCNSSV--KSSLNMVLVDKEAW----GEDSGLAF 277

Qy 839 ---LLNSRTNGNVH--HKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACL 893
Db 278 FRCLIDLRLKGTLSKWQTMKPFLLAGSITPADSDCLRLAGYSNS-IRKPLRLSTVAACL 336

Qy 894 QQVLELRKTRQQHPGEGSPATLKSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCAS 953
Db 337 SKALGVGLTGRRRSDNS--LVLRSVLTGKNILVDDNAVNRIVAAGALKKYGAIVTCVDS 394

Qy 954 GOVALGLLQIPHTEFACFMDIQMPQMDGFEATRQIRMEKEAKEK-----TNL 1001
Db 395 GKRAISRLQPPHKFDACFMDVQMPMDGFEATRLVRSVESKINDTIQAGEVSSEIYGNKA 454

Qy 1002 EWHLPILAMTADVIHATYEECLKSGMDGYVSKPFEENLYKSVAKSFKPN 1051
Db 455 HWHVPILAMTADVIQATFE-----GSSAKNPFQDNNIAKQ--KSYAVN 495

RESULT 15
Q8EII0 PRELIMINARY; PRT; 1765 AA.
ID Q8EII0

AC	Q8EII10;	
DT	01-MAR-2003 (TrEMBLrel. 23, Created)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	
DE	Sensory box histidine kinase/response regulator.	
GN	SO0859.	
OS	Shewanella oneidensis.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;	
OC	Alteromonadaceae; Shewanella.	
OX	NCBI_TaxID=70863;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=MR-1;	
RX	MEDLINE=22297686; PubMed=12368813;	
RA	Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,	
RA	Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,	
RA	Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,	
RA	DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,	
RA	Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,	
RA	Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,	
RA	Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,	
RA	Feldblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;	
RT	"Genome sequence of the dissimilatory metal ion-reducing bacterium	
RT	Shewanella oneidensis.";	
RL	Nat. Biotechnol. 20:1118-1123(2002).	
DR	EMBL; AE015531; AAN53935.1; -.	
DR	TIGR; SO0859; -.	
KW	Kinase; Complete proteome.	
SQ	SEQUENCE 1765 AA; 197093 MW; 64DFF9AD82B24D90 CRC64;	
Query Match 14.9%; Score 806.5; DB 16; Length 1765;		
Best Local Similarity 26.4%; Pred. No. 2e-43;		
Matches 266; Conservative 165; Mismatches 338; Indels 237; Gaps 30;		
Qy	95 TFIQHRALLPKALILWIIIVG---FISSGIYQWMDA-----NKIRREEVLVSMCDQR 145	
Db	717 TFEVEYRIRHRDGSIRWVHEKGKASYSEEGPLWFDGSIDDVTESKLAIDEI-----EA 770	
Qy	146 ARMLQDQFSVSVNHVHALAILVSTFHYHKNPSAIDQETFAEYRTARTAFERPLLSGVAYAE 205	
Db	771 SRQQLTNITESI-----PCTVYQLRWVPTDRSF---TFLSGAALA- 808	
Qy	206 KVVNFEREMFERQHNWVIKTMDRGEPSVRDEYAPVIFSQDSVSYLESLDMMSGEEDREN 265	
Db	809 -MLGLHREELLRDFNIIAER-----IPDEERP-----EVISALAGKSD-DQ 847	
Qy	266 ILRARETGKAVLTSPFRLLETHHLGVV-----LTFPVYKSSLPENPTVEERIAATAGYLG 320	
Db	848 LRWIREFRYRHPNGGIRWMEAGASGHYADDGSIWNGYVMDVTERKSIEEELAVSEAHFK 907	
Qy	321 GAF-----DVESLVENLLGQ-----LAGNQAIVVHVYDITNASDPLVMYGNQDE 364	
Db	908 ALPDGATIGIVNVDIKGLILDNCNYQFCEDMGLSRDELSTPIFDVLSAQDKDVAKAQFKE 967	
Qy	365 EADRSLSHESKLDFGDPFRKHKMICRYHQKAPIPLNVLTVPLFFAIGFLVGYYILYGAAM 424	
Db	968 LVEGKIDH-----YRGERSFVRPSGE-----PLWMTVN-----VS 997	
Qy	425 HIVKVEDDFH-----EMQELKV-----RAEAAADVAKSQFLATVSHETRPMNG 467	
Db	998 TLLDSQNQFESAVVSMVDMTELKLLSDELLVAKDEADAASKAKGDFLANMSHEIRTPMNA 1057	
Qy	468 ILGMLAMLLDTELSSTQRDYAQTAVCGKALIALINEVLDRAKIEAGKLELESVPFFIRS 527	
Db	1058 IIGMSQLCLQTQLDKKQKNYLEKIERASQSLSIINDILDFSKIEAGKLDIENVSFQDIT 1117	
Qy	528 ILDDVLSLFSSESRNKGIELAVFVSDKVPEIVKGDGSRFRQIIINLVGNSVKFTEKGHIF 587	
Db	1118 MLEDLSDMFSERAAQKQIELLFVAVPNVPHLLGDPRLGLQVLINLMNNAIKFTERGEVL 1177	
Qy	588 VKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQSSYNTLSGYEAADGRNSWDSFKHLVSE 647	
Db	1178 LSLSLVEQQNDD----- 1189	

Qy	648 EQSLSEFDISSNVRMLMVSIEDTGIGIPLVAQQRVNPFMQADSSSTRNYGGTGIGISISK 707	
Db	1190 -----VVLRFVVRDSGIGLTQEQQSKLPKSFQTQADTSTTRKYGGTGLGLAISK 1237	
Qy	708 CLVELMRGOINFISRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSSTFKGMKAIVV 767	
Db	1238 QLVELMGSGIGVESQLGHGSTFFFTVKL-----CISSGQKLFV---GQELDGMNSILVA 1287	
Qy	768 DAKPVRAAVTRYHMKRLGINVDVVTSLKTAVVAAAAAFERNGSPLPTK-PQLDMILVEKDS 826	
Db	1288 DDNATARDIMRTTLESMGFNVDTVRSGDEAIMRCSQOEYAYALIDWKMPNLDGIETAKQI 1347	
Qy	827 WISTEDNDSEIRLLNSRTNGNVVHKSPKLALFATNITNSEFDRAKSAGFADTVINKPLRA 886	
Db	1348 KQQTK-NAPRILMVSAHANQD-----FLTQI-----EQLGLAGY-----ISKPISA 1387	
Qy	887 S-----MIGACLOQVLELRKTRQQHPGSSSPATLKSLLTGKKILVDDNIVNRRAAGA 940	
Db	1388 SRLLDGINNALGRSGILPVR-----HQDNIAPELLLP-LKGKRILLVEDNEMNLEVATEF 1442	
Qy	941 LKKFGEAEVVCESGGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQIRMMKEAKEKTN 1000	
Db	1443 LEQVGIIILSIATNGQIALDKL-AQQSFDLVLMDCQMPVMDGYQATKAIRQRPDLAQ---- 1497	
Qy	1001 LEWHLPILAMTADVIHATYEECLKSGMDGYVSKPFEENLYKSVAK 1046	
Db	1498 ----LPVIAMTANAMAGDKEMCLRAGMNDHIAKPIEVNLLYQTLTK 1539	

Search completed: November 28, 2003, 14:05:05
Job time : 38.4302 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 13:58:18 ; Search time 39.5984 Seconds
(without alignments)
4236.886 Million cell updates/sec

Title: US-09-918-508-6
Perfect score: 5397
Sequence: 1 MNWALNNHQEEEEPRRIEI.....ENLYKSVAKSFKNPISPSS 1057

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	5397	100.0	1057	23	ABG70783	A. thaliana cytoki
2	5387	99.8	1057	23	AAO22558	Wooden leg (WOL) g
3	5387	99.8	1057	24	AAE33694	Arabidopsis thalia
4	5383	99.7	1057	23	AAO22570	Wooden leg (WOL) g
5	5382	99.7	1057	24	AAE33696	Arabidopsis thalia
6	5379	99.7	1057	24	AAE33695	Arabidopsis thalia
7	2865	53.1	600	23	ABH91688	Herbicidally activ
8	2546	47.2	1132	21	AAG47090	Arabidopsis thalia
9	2546	47.2	1176	21	AAG47089	Arabidopsis thalia

10	2546	47.2	1176	23	ABG70781	A. thaliana cytoki
11	2546	47.2	1176	24	AAE33692	Arabidopsis thalia
12	2546	47.2	1238	21	AAG47088	Arabidopsis thalia
13	2534.5	47.0	1173	23	AAO22568	Wooden leg (WOL) g
14	2534.5	47.0	1173	23	ABB93625	Herbicidally activ
15	2485	46.0	1036	23	ABG70782	A. thaliana cytoki
16	2485	46.0	1036	24	AAE33693	Arabidopsis thalia
17	2402	44.5	1092	23	AAO22567	Wooden leg (WOL) g
18	2402	44.5	1092	23	ABH91150	Herbicidally activ
19	1434	26.6	289	23	AAO22563	Wooden leg (WOL) g
20	1415	26.2	274	23	AAO22561	Wooden leg (WOL) g
21	1248	23.1	412	21	AAE33694	Eucalyptus grandis
22	993	18.4	426	21	AAE33695	Eucalyptus grandis
23	702	13.0	2150	23	AAO22566	Wooden leg (WOL) g
24	668	12.4	1081	20	AAO22564	cos-1 histidine ki
25	664	12.3	1081	20	AAW81600	Candida albicans C
26	661	12.2	132	23	AAO22564	Wooden leg (WOL) g
27	654	12.1	1298	19	AAW68522	N. crassa oslp pro
28	654	12.1	1298	20	AAO22564	osl+p amino acid s
29	652	12.1	1281	20	AAO22564	osl histidine kina
30	652	12.1	1298	20	AAO22564	osl histidine kina
31	632	11.7	123	23	AAO22565	Wooden leg (WOL) g
32	616	11.4	971	20	AAW88480	Candida albicans h
33	616	11.4	2471	20	AAW88481	Candida albicans h
34	594.5	11.0	922	22	AAO22564	Histidine protein k
35	594.5	11.0	922	22	AAO22564	Histidine protein k
36	588.5	10.9	922	22	AAO22564	Histidine protein k
37	585	10.8	1018	21	AAO22564	Eucalyptus grandis
38	577.5	10.7	816	21	AAO22564	Eucalyptus grandis
39	571.5	10.6	950	23	ABB93422	Herbicidally activ
40	571	10.6	1122	23	ABB92150	Herbicidally activ
41	551	10.2	105	23	AAO22559	Wooden leg (WOL) g
42	541	10.0	747	24	ABU03033	Moss lipid metabol
43	531.5	9.8	1146	20	AAW86007	Histidine kinase C
44	517	9.6	185	21	AAO22564	Pinus radiata cell
45	503.5	9.3	496	24	AAO26995	Pseudomonas aerugi

ALIGNMENTS

RESULT 1
ABG70783
ID ABG70783 standard; Protein; 1057 AA.
XX
AC ABG70783;
XX
DT 09-DEC-2002 (first entry)
XX
DE A. thaliana cytokinin receptor, CRE1, protein.
XX
KW CRE1; plant; antagonist; agonist; cytokinin receptor;
KW receptor; signal transduction; histidine kinase; hormone; cell division;
KW cell differentiation; agriculture; growth regulator; harvest.
XX
OS Arabidopsis thaliana.
XX
PN EPI241182-A2.
XX
PD 18-SEP-2002.
XX
PF 13-MAR-2002; 2002EP-0005749.
XX
PR 15-MAR-2001; 2001JP-0073812.
PR 29-JUN-2001; 2001JP-0198639.
PR 29-JUN-2001; 2001JP-0198640.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Kakimoto T, Higuchi M, Inoue T;
XX
DR WPI; 2002-693041/75.
DR N-PSDB; ABS54452.

XX Analyzing agonist or antagonist activity of a substance for use as a
PT plant growth regulator, comprises measuring intracellular signal
PT transduction from a cytokinin receptor expressed in a cell contacted
PT with the test substance -
XX
PS Claim 1; Page 39-41; 47pp; English.
XX
CC The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor
CC region is heterogeneous to them. Cytokinins are plant hormones relevant
CC to cell division and differentiation of higher plants. The method is used
CC for analysing agonist or antagonist activity to a cytokine receptor. A
CC substance with agonist or antagonist activity to the receptor can be
CC used, in agriculture, as a plant growth regulator, e.g. after harvest.
CC The advantage is that the candidate substances do not need to be prepared
CC in such large amounts as in previous methods and that the method avoids
CC the immensely long time to observe and evaluate the growth of the plant
CC and the physiological changes of the plant after spraying. The sequence
CC presented is the A. thaliana cytokinin receptor, CRE1, protein.
XX
SQ Sequence 1057 AA;

Query Match 100.0%; Score 5397; DB 23; Length 1057;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1057; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNWALNNHQEEEPRIEISDSSELENLKSSDFYQLGGGALNSEKPRKIDFWRSGLM 60
Db 1 MNWALNNHQEEEPRIEISDSSELENLKSSDFYQLGGGALNSEKPRKIDFWRSGLM 60
QY 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFQIHRALLPKALILWIIIVGFSS 120
Db 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFQIHRALLPKALILWIIIVGFSS 120
QY 121 GIYQWMDANKIRREEVLSVCMCDQARMQDQPSVSNVHVHALAILVSTFHYHKNPSAID 180
Db 121 GIYQWMDANKIRREEVLSVCMCDQARMQDQPSVSNVHVHALAILVSTFHYHKNPSAID 180
QY 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240
Db 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240
QY 241 VIFSQDSVSYLESMDMSGEEDRENILRARETGKAVLTSPFRLLETHHLGWLTFFPVYKS 300
Db 241 VIFSQDSVSYLESMDMSGEEDRENILRARETGKAVLTSPFRLLETHHLGWLTFFPVYKS 300
QY 301 SLPENPTVEERIAATAGYLGGAFFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYG 360
Db 301 SLPENPTVEERIAATAGYLGGAFFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYG 360
QY 361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTPVLPFFAIGFLVGYYLY 420
Db 361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTPVLPFFAIGFLVGYYLY 420
QY 421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480
Db 421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480
QY 481 SSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540
Db 481 SSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540
QY 541 RNKGIELAVFSDKVPEIVKGDGSRFRQIILNLVGNVSKFTEKGHIFVKVHLAEQSKDES 600
Db 541 RNKGIELAVFSDKVPEIVKGDGSRFRQIILNLVGNVSKFTEKGHIFVKVHLAEQSKDES 600

QY 601 EPKNALNGGVSEEMIVVSKOSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660
Db 601 EPKNALNGGVSEEMIVVSKOSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660
QY 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSSSTRNYGGTGIGLSISKCLVELMRGQINF 720
Db 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSSSTRNYGGTGIGLSISKCLVELMRGQINF 720
QY 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAIIVDAKPVRAAVTRYH 780
Db 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAIIVDAKPVRAAVTRYH 780
QY 781 MKRLGINVDVVTSLKTAVVAAAFAFERNGSPLPTKPOLDMILVEKDSWISTEDNDSEIRLL 840
Db 781 MKRLGINVDVVTSLKTAVVAAAFAFERNGSPLPTKPOLDMILVEKDSWISTEDNDSEIRLL 840
QY 841 NSRTNGNVHHKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELR 900
Db 841 NSRTNGNVHHKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELR 900
QY 901 KTRQHPGEGSSPATLKSLLTGKILVVDNINVRRVAGALKKFGAEVVCESGOVALGL 960
Db 901 KTRQHPGEGSSPATLKSLLTGKILVVDNINVRRVAGALKKFGAEVVCESGOVALGL 960
QY 961 LQIPHTFDACFMDIQMPQMDGFATRQIRMMEKEAKEKTNLEWHLPILAMTADVIHATYE 1020
Db 961 LQIPHTFDACFMDIQMPQMDGFATRQIRMMEKEAKEKTNLEWHLPILAMTADVIHATYE 1020
QY 1021 ECLKSGMDGYVSKPFEENLYKSVAKSKPNPISPSS 1057
Db 1021 ECLKSGMDGYVSKPFEENLYKSVAKSKPNPISPSS 1057

RESULT 2
AAO22558
ID AAO22558 standard; Protein; 1057 AA.
XX

AC AAO22558;

DT 28-OCT-2002 (first entry)

XX Wooden leg (WOL) gene related protein SEQ ID No 5.

DE Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
KW wood production; plant; promoter; tree; crop plant.

OS Arabidopsis thaliana.

XX WO200244337-A2.

PD 06-JUN-2002.

XX 29-NOV-2001; 2001WO-US45053.

PR 29-NOV-2000; 2000US-253739P.

PA (UINY) UNIV NEW YORK STATE.

PA (HELA/) HELARIUTTA Y.

PA (MAHO/) MAHONEN A P.

PA (BONK/) BONKE A W M.

PA (KAUP/) KAUPPINEN L.

PA (RIIK/) RIIKONEN M.

XX Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;

PI Benfey PN;

XX WPI; 2002-599423/64.

DR Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set

XX of asymmetric cell divisions that establish vascular tissue in root and

PT hypocotyl development, useful for improving agronomically valuable

PT plants -

XX	Claim 6; Fig 5D; 187pp; English.	601	EPKNALNGGVSEEMIVVSKQSSYNTLSGYEADGRNSWDSFKHLVSEEQSLSEFDISSNV	660
PS				
XX		601	EPKNALNGGVSEEMIVVSKQSSYNTLSGYEADGRNSWDSFKHLVSEEQSLSEFDISSNV	660
CC	The invention relates to an isolated WOODEN LEG (WOL) polypeptide, comprising 15 contiguous amino acids of a fully defined Arabidopsis WOODEN LEG protein sequence of 1057 amino acids as given in the specification, and to its encoding nucleic acid. The invention also relates to an amino acid sequence of domains of protein, e.g., N-terminal region, C-terminal domain, etc; or is a naturally occurring allelic variant of the above mentioned polypeptide sequence. Expression levels of the nucleic acid can be modified to improve the vasculature in transgenic plants and enhance the agronomic properties of such plants. Also the WOL promoter is used to drive expression of a heterologous coding sequence of trees to improve wood production. The WOL nucleic acid may be used as a molecular marker for a qualitative trait loci, e.g., longer roots or enhanced wood production, in molecular breeding of crop plants. The nucleic acid is also useful in DNA amplification assays to identify the endogenous WOL genes, WOL mutant alleles and/or WOL expression products in cultivars as compared to wild-type plants. They can also be used as markers for linkage analysis of qualitative trait loci. The WOL protein and/or antibodies can be used as diagnostic reagents in immunoassays to detect expression of the WOL gene in cultivars and wild-type plants. The WOL protein, its encoding nucleic acid, and its corresponding antibody are useful for improving agronomically valuable plants e.g., trees. This sequence represents a protein relating to the wooden leg (WOL) protein of the invention.	661	RLMVSIEDTGIGIPLVAQGRVFMFMQADSSTSRNYGGTGIGISISKCLVELMRGQINFI	720
CC				
CC		661	RLMVSIEDTGIGIPLVAQGRVFMFMQADSSTSRNYGGTGIGISISKCLVELMRGQINFI	720
CC				
CC		721	SRPHIGSTFWPTAVLEKCDKCSAINHMKKPNVEHLPSTFKGMKAIVVDKPVRAAVTRYH	780
CC				
CC		721	SRPHIGSTFWPTAVLEKCDKCSAINHMKKPNVEHLPSTFKGMKAIVVDKPVRAAVTRYH	780
CC				
CC		781	MKRLGINVDVVTSLKTAVVAAAFAFERNGLPTKPLQDMLILVEKDSWISTEDNDSEIRLL	840
CC				
CC		781	MKRLGINVDVVTSLKTAVVAAAFAFERNGLPTKPLQDMLILVEKDSWISTEDNDSEIRLL	840
CC				
CC		841	NSRTNGNVHKKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMGACLQQVLELR	900
CC				
CC		841	NSRTNGNVHKKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMGACLQQVLELR	900
CC				
CC		901	KTRQOHPEGSSPATLKSLLTGKILVVDDNIVNRRVAAGALKKFGAEVVCESGOVALGL	960
CC				
CC		901	KTRQOHPEGSSPATLKSLLTGKILVVDDNIVNRRVAAGALKKFGAEVVCESGOVALGL	960
CC				
CC		961	LQIPHFTDFACFMDIQMPQMDGFATRQIRMMEKEAKEKTNLEWHLPILAMTADVIHATYE	1020
CC				
CC		961	LQIPHFTDFACFMDIQMPQMDGFATRQIRMMEKETKEKTNLEWHLPILAMTADVIHATYE	1020
XX				
SQ	Sequence 1057 AA;	1021	ECLKSGMDGYVSKPFEEENLYKSVAKSFKNPISPSS	1057
	Query Match 99.8%; Score 5387; DB 23; Length 1057;	1021	ECLKSGMDGYVSKPFEEENLYKSVAKSFKNPISPSS	1057
	Best Local Similarity 99.8%; Pred. No. 0;			
	Matches 1055; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	1 MNWALNNHQEEEEPRRIEISDSELENLKSSDFYQLGGGALNSSEKPRKIDFWRSGLM	RESULT 3		
Db	1 MNWALNNHQEEEEPRRIEISDSELENLKSSDFYQLGGGALNSSEKPRKIDFWRSGLM	AAE33694		
QY	61 GFAMQOQQQLQHSVAVKMNNNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFISS	ID AAE33694 standard; Protein; 1057 AA.		
Db	61 GFAMQOQQQLQHSVAVKMNNNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFISS	XX AAE33694;		
QY	121 GIYQWMDANKIRREEVLVSMCDQARMLOQFSVSNVHVHALAILVSTFHYHKNPSAID	AC AAE33694;		
Db	121 GIYQWMDANKIRREEVLVSMCDQARMLOQFSVSNVHVHALAILVSTFHYHKNPSAID	XX 16-APR-2003 (first entry)		
QY	181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWIKTMDRGESPVRDEYAP	XX Arabidopsis thaliana histidine kinase 4 (AHK4)-WOL, CRE1 protein.		
Db	181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWIKTMDRGESPVRDEYAP	XX Shoot formation; senescence; transgenic; transgenic plant; agriculture; cell proliferation; shoot meristem formation; leaf development; AHK; photosynthesis; histidine kinase; enzyme; CRE1.		
QY	241 VIFSQDSVSVLESDDMSGEEDRENILRARETGKAVLTSPFRLLETHLGVVLTFFPVYKS	OS Chimeric - Arabidopsis thaliana.		
Db	241 VIFSQDSVSVLESDDMSGEEDRENILRARETGKAVLTSPFRLLETHLGVVLTFFPVYKS	OS Chimeric - Unidentified.		
QY	301 SLPENPTVEERIAATAGYLGGAFFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYG	XX WO200299079-A2.		
Db	301 SLPENPTVEERIAATAGYLGGAFFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYG	PD 12-DEC-2002.		
QY	361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTVPFFAIGFLVGIIYLY	XX 06-JUN-2002; 2002WO-US18066.		
Db	361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTVPFFAIGFLVGIIYLY	XX 06-JUN-2001; 2001US-296554P.		
QY	421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL	PA (GEHO) GEN HOSPITAL CORP.		
Db	421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL	XX Sheen J, Hwang I;		
QY	481 SSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES	PI WPI; 2003-140613/13.		
Db	481 SSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES	XX Increasing yield in plant, increasing shoot formation in a plant, or delaying senescence in a plant such as wheat, rice, maize, barley, potato, by using transgenes that regulate cytokinin response -		
QY	541 RNKGIELAVFVSDKVPEIVKGDGRFRQIINLVGNSVKFTEKGHIFVKVHLAEQSKDES	PS Disclosure; Page 80-82; 87pp; English.		
Db	541 RNKGIELAVFVSDKVPEIVKGDGRFRQIINLVGNSVKFTEKGHIFVKVHLAEQSKDES	XX The present invention relates to a novel method of increasing yield in a plant, increasing shoot formation or delaying senescence in a plant. The method involves introducing into plant cells, a transgene having a B-type		

CC response regulator operably linked to a promoter functional in plant
CC cells to yield transformed plant cells or whose expression reduces the
CC expression of A-type response regulator in the cells of the plant and
CC regenerating a plant from the transformed cells. The method is useful
CC for increasing the yield in a plant, increasing the shoot formation or
CC delaying senescence in a plant such as wheat, rice, maize, barley,
CC potato, tomato, soybean, tomato, oat, cotton and sunflower. The method
CC is useful for variety of agricultural and commercial purposes including
CC improving and enhancing photosynthesis, promoting cell proliferation,
CC shoot meristem formation, promoting leaf development, increasing crop
CC yields, improving crop and ornamental quality and reducing agricultural
CC production costs. The present sequence is Arabidopsis thaliana histidine
CC kinase 4 (AHK4)-WOL, CRE1 protein. This sequence is used to illustrate
CC the method of the invention.

SQ Sequence 1057 AA;
Query Match 99.8%; Score 5387; DB 24; Length 1057;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1055; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNWALNNHQEEBEPRIEISDSSELENLKSSDFYQLGGGALNSEKPRKIDFWRSGLM 60
Db 1 MNWALNNHQEEBEPRIEISDSSELENLKSSDFYQLGGGALNSEKPRKIDFWRSGLM 60
QY 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFSS 120
Db 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFSS 120
QY 121 GIYQWMDANKIRREEVLSVCMCDQARMLODQFSVSNHVHALAILVSTFHYKNPSAID 180
Db 121 GIYQWMDANKIRREEVLSVCMCDQARMLODQFSVSNHVHALAILVSTFHYKNPSAID 180
QY 181 QETFAEYRTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240
Db 181 QETFAEYRTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240
QY 241 VIFSQDSVSYLESDDMSGEEDRENILRARETGKAVLTSPFRLLETHHLGVLTFFPVYKS 300
Db 241 VIFSQDSVSYLESDDMSGEEDRENILRARETGKAVLTSPFRLLETHHLGVLTFFPVYKS 300
QY 301 SLPENPTVEERIAATAGYLGGAFDVESILVENLLGQLAGNQAIIVHVYDITNASDPLVMYG 360
Db 301 SLPENPTVEERIAATAGYLGGAFDVESILVENLLGQLAGNQAIIVHVYDITNASDPLVMYG 360
QY 361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTVPLFFAIGFLVGYYLY 420
Db 361 NQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPLNVLTTVPLFFAIGFLVGYYLY 420
QY 421 GAAMHIVKVEDDFHEMOELKVRAEAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480
Db 421 GAAMHIVKVEDDFHEMOELKVRAEAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480
QY 481 SSTQDYAQTAAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540
Db 481 SSTQDYAQTAAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540
QY 541 RNKGIELAVFVSDKVPEIVKGDGSRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600
Db 541 RNKSIELAVFVSDKVPEIVKGDGSRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600
QY 601 EPKNALNGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660
Db 601 EPKNALNGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660
QY 661 RLMVSIEDTGIGIPLVAQGRVEMPFMQADSSSTRNYGGTGIGISISKCLVELMRGQINFI 720
Db 661 RLMVSIEDTGIGIPLVAQGRVEMPFMQADSSSTRNYGGTGIGISISKCLVELMRGQINFI 720
QY 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPSTFTKGMKAIVVDKPVRAAVTRYH 780
Db 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPSTFTKGMKAIVVDKPVRAAVTRYH 780

QY 781 MKRLGINVDVVTSLKTAVVAAAFAERNGSPLTPKPQLDMILVEKDSWISTEDNDSEIRLL 840
Db 781 MKRLGINVDVVTSLKTAVVAAAFAERNGSPLTPKPQLDMILVEKDSWISTEDNDSEIRLL 840
QY 841 NSRTNGNVHHSKPKLALFATNITNSEFDRAKSAGFADTVMKPLRASMIGACLOQVLELR 900
Db 841 NSRTNGNVHHSKPKLALFATNITNSEFDRAKSAGFADTVMKPLRASMIGACLOQVLELR 900
QY 901 KTRQHPGEGSSPATLKSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCESGQVALGL 960
Db 901 KTRQHPGEGSSPATLKSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCESGQVALGL 960
QY 961 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKEAKEKTNLEWHLPILAMTADVIHATYE 1020
Db 961 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKETKEKTNLEWHLPILAMTADVIHATYE 1020
QY 1021 ECLKSGMDGYVSKPFEEENLYKSVAKSFKNPISPSS 1057
Db 1021 ECLKSGMDGYVSKPFEEENLYKSVAKSFKNPISPSS 1057

RESULT 4
AAO22570

ID AAO22570 standard; Protein; 1057 AA.

XX AAO22570;

XX 28-OCT-2002 (first entry)

XX Wooden leg (WOL) gene related protein SEQ ID No 24.

XX Wooden leg; WOL; vasculature; transgenic plant; agronomic; longer root;
XX wood production; plant; promoter; tree; crop plant.

XX Arabidopsis thaliana.

XX WO200244337-A2.

XX 06-JUN-2002.

XX 29-NOV-2001; 2001WO-US45053.

XX 29-NOV-2000; 2000US-253739P.

XX (UJNY) UNIV NEW YORK STATE.

XX (HELA/) HELARIUTTA Y.

XX (MAHO/) MAHONEN A P.

XX (BONK/) BONKE A W M.

XX (KAUP/) KAUPPINEN L.

XX (RIIK/) RIIKONEN M.

PI Helariutta Y, Mahonen AP, Bonke AW, Kauppinen L, Riikonen M;

XX Benfey PN;

XX WPI; 2002-599423/64.

XX Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set

XX of asymmetric cell divisions that establish vascular tissue in root and

XX hypocotyl development, useful for improving agronomically valuable

XX plants -

PS Disclosure; Page 167-171; 187pp; English.

XX The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
XX comprising 15 contiguous amino acids of a fully defined Arabidopsis
XX WOODEN LEG protein sequence of 1057 amino acids as given in the
XX specification, and to its encoding nucleic acid. The invention also
XX relates to an amino acid sequence of domains of protein, e.g., N-terminal
XX region, C-terminal domain, etc; or is a naturally occurring allelic
XX variant of the above mentioned polypeptide sequence. Expression levels of
XX the nucleic acid can be modified to improve the vasculature in transgenic
XX plants and enhance the agronomic properties of such plants. Also the WOL
XX promoter is used to drive expression of a heterologous coding sequence of

CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.

XX Sequence 1057 AA;

Query Match 99.7%; Score 5383; DB 23; Length 1057;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1054; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNWALNNHQEEEEPRRIEISDESLENLKSSDFYQLGGGALNSSEKPRKIDFWRSGIM 60
Db 1 MNWALNNHQEEEEPRRIEISDESLENLKSSDFYQLGGGALNSSEKPRKIDFWRSGIM 60
QY 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHALLPKALILWIIIVGFSS 120
Db 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHALLPKALILWIIIVGFSS 120
QY 121 GIQWMDANKIRREEVLVSMCDQARMLODQFSVSNVHVALAILVSTFHYHKNSAID 180
Db 121 GIQWMDANKIRREEVLVSMCDQARMLODQFSVSNVHVALAILVSTFHYHKNSAID 180
QY 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240
Db 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTMDRGEPSPVRDEYAP 240
QY 241 VIFSQDSVSYLESIDMSGEEDRENILRARETGKAVLTSPRLLETHHLGVVLTFFPVYKS 300
Db 241 VIFSQDSVSYLESIDMSGEEDRENILRARETGKAVLTSPRLLETHHLGVVLTFFPVYKS 300
QY 301 SLPENPTVEERIAATAGYLGGAFFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYG 360
Db 301 SLPENPTVEERIAATAGYLGGAFFDVESLVENLLGQLAGNQAIVVHVYDITNASDPLVMYG 360
QY 361 NQDEEADRSLSHESKLDGDFPRKHKMICRYHQKAPIPLNVLTTPVLPFFAIGFLVGILY 420
Db 361 NQDEEADRSLSHESKLDGDFPRKHKMICRYHQKAPIPLNVLTTPVLPFFAIGFLVGILY 420
QY 421 GAAWHIVKVEDDFHEMQELKVRAEAADVAKSQFLATVSHEIRTPMNGILGLMLLDTEL 480
Db 421 GAAWHIVKVEDDFHEMQELKVRAEAADVAKSQFLATVSHEIRTPMNGILGLMLLDTEL 480
QY 481 SSTQRDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540
Db 481 SSTQRDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSEES 540
QY 541 RNKGIELAVFVSDKVPEIVKGDGSRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600
Db 541 RNKSIELAVFVSDKVPEIVKGDGSRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600
QY 601 EPKNALNGGVSEEMIVVSKOSSYNLTSGYEAAADGRNSWDSFKHLVSEEQSLSEEDISSNV 660
Db 601 EPKNALNGGVSEEMIVVSKOSSYNLTSGYEAAADGRNSWDSFKHLVSEEQSLSEEDISSNV 660
QY 661 RLMVSIEDTGIGIPLVAQGRVFMFPFMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI 720
Db 661 RLMVSIEDTGIGIPLVAQGRVFMFPFMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI 720
QY 721 SRPHIGSTFWFTAVLEKCKCSAINHMKPNVEHLPSTFKGMKAIIVDAKPVRAAVTRYH 780
Db 721 SRPHIGSTFWFTAVLEKCKCSAINHMKPNVEHLPSTFKGMKAIIVDAKPVRAAVTRYH 780
QY 781 MKRLGINVDVVTSLKTAVVAAAAAFERNGSPLPTKPQLDMILVEKDSWISTEDNDSEIRLL 840

Db 781 MKRLGINVDVVTSLKTAVVAAAAAFERNGSPLPTKPQLDMILVEKDSWISTEDNDSEIRLL 840
QY 841 NSRTNGNVHHKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLOQVLELR 900
Db 841 NSRTNGNVHHKSPKLALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLOQVLELR 900
QY 901 KTRQHQHEGSSPATLKSLLTGKKILVDDNIVNRRRVAAGALKKFGAEVVCAESGQVALGL 960
Db 901 KTRQHQHEGSSPATLKSLLTGKKILVDDNIVNRRRVAAGALKKFGAEVVCAESGQVALGL 960
QY 961 LQIPHTFDACFMDIQMPQMDGFEATQIRMEKEAKEKTNLEWHLPILAMTADVIAHYE 1020
Db 961 LQIPHTFDACFMDIQMPQMDGFEATQIRMEKEAKEKTNLEWHLPILAMTADVIAHYE 1020
QY 1021 ECLKSGMDGYVSKPFEEENLYKSVAKSFKNPISPSS 1057
Db 1021 ECLKSGMDGYVSKPFEEENLYKSVAKSFKNPISPSS 1057
RESULT 5
AAE33696
ID AAE33696 standard; Protein; 1057 AA.
XX
AC AAE33696;
XX
DT 16-APR-2003 (first entry)
XX
DE Arabidopsis thaliana CRE1 mutant (D973N) protein.
XX
KW Shoot formation; senescence; transgenic; transgenic plant; agriculture;
KW cell proliferation; shoot meristem formation; leaf development;
KW photosynthesis; CRE1; mutant; mutein.
XX
OS Arabidopsis thaliana.
OS Synthetic.
XX
PN WO200299079-A2.
XX
PD 12-DEC-2002.
XX
PF 06-JUN-2002; 2002WO-US18066.
XX
PR 06-JUN-2001; 2001US-296554P.
XX (GEO) GEN HOSPITAL CORP.
PI Sheen J, Hwang I;
XX
DR WPI; 2003-140613/13.
XX
PT Increasing yield in plant, increasing shoot formation in a plant, or
PT delaying senescence in a plant such as wheat, rice, maize, barley,
PT potato, by using transgenes that regulate cytokinin response -
XX
PS Disclosure; Page 85-87; 87pp; English.
XX
CC The present invention relates to a novel method of increasing yield in a
CC plant, increasing shoot formation or delaying senescence in a plant. The
CC method involves introducing into plant cells, a transgene having a B-type
CC response regulator operably linked to a promoter functional in plant
CC cells to yield transformed plant cells or whose expression reduces the
CC expression of A-type response regulator in the cells of the plant and
CC regenerating a plant from the transformed cells. The method is useful
CC for increasing the yield in a plant, increasing the shoot formation or
CC delaying senescence in a plant such as wheat, rice, maize, barley,
CC potato, tomato, soybean, tomato, oat, cotton and sunflower. The method
CC is useful for variety of agricultural and commercial purposes including
CC improving and enhancing photosynthesis, promoting cell proliferation,
CC shoot meristem formation, promoting leaf development, increasing crop
CC yields, improving crop and ornamental quality and reducing agricultural
CC production costs. The present sequence is Arabidopsis thaliana CRE1
CC mutant protein. This sequence is used to illustrate the method of the

QY 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFISS 120
Db 61 GFAKMQQQQLQHSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKALILWIIIVGFISS 120
QY 121 GIYQWMDANKIRREEVLVSMCDQARMQLQDQFSVNVHVALAILVSTFHYHKNPSSAID 180
Db 121 GIYQWMDANKIRREEVLVSMCDQARMQLQDQFSVNVHVALAILVSTFHYHKNPSSAID 180
QY 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNVVVKTMDRGEPSPVRDEYAP 240
Db 181 QETFAEYTARTAFERPLLSGVAYAEKVNVFEREMFERQHNVVVKTMDRGEPSPVRDEYAP 240
QY 241 VIFSQDSVSYLESLDMMSGEEDRENILRARETGKAVLTSPFRLLLETHHLGVVLTFFPVYKS 300
Db 241 VIFSQDSVSYLESLDMMSGEEDRENILRARETGKAVLTSPFRLLLETHHLGVVLTFFPVYKS 300
QY 301 SLPENPTVEERIAATAGYLGAFDVESLVENLLGQAGNQAIWVHYDITNASDPLVMYG 360
Db 301 SLPENPTVEERIAATAGYLGAFDVESLVENLLGQAGNQAIWVHYDITNASDPLVMYG 360
QY 361 NQDEEADRSLSHESKLDGDFPRKHKMICRYHQKAPIPLNVLTTPVLFFAIGFLVGYILY 420
Db 361 NQDEEADRSLSHESKLDGDFPRKHKMICRYHQKAPIPLNVLTTPVLFFAIGFLVGYILY 420
QY 421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480
Db 421 GAAMHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTEL 480
QY 481 SSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSSEES 540
Db 481 SSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSSEES 540
QY 541 RNKGIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600
Db 541 RNKSIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDES 600
QY 601 EPKNALNGGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660
Db 601 EPKNALNGGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNV 660
QY 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI 720
Db 661 RLMVSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI 720
QY 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAIVVDKPVRAAVTRYH 780
Db 721 SRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAIVVDKPVRAAVTRYH 780
QY 781 MKRLGINVDVVTSLKTAVVAAAAAFERNGPSPLTPKPQLDMILVEKDSWISTEDNDSEIRLL 840
Db 781 MKRLGINVDVVTSLKTAVVAAAAAFERNGPSPLTPKPQLDMILVEKDSWISTEDNDSEIRLL 840
QY 841 NSRTNGNVHKSPLKALFATNITNSEFDRAKSAGFADTVIMKPLRASMTGACLQQVLELR 900
Db 841 NSRTNGNVHKSPLKALFATNITNSEFDRAKSAGFADTVIMKPLRASMTGACLQQVLELR 900
QY 901 KTRQOHPEGSSPATLKSLLTGKKILVVDNIVNRRVAAGALKKFGAEVVCABSGQVALGL 960
Db 901 KTRQOHPEGSSPATLKSLLTGKKILVVDNIVNRRVAAGALKKFGAEVVCABSGQVALGL 960
QY 961 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKAKEKTNLEWHLPILAMTADVIHATYE 1020
Db 961 LQIPHTFDACFMDIQMPQMDGFEATRQIRMMEKETKEKTNLEWHLPILAMTADVIHATYE 1020
QY 1021 ECLKSGMDGYVSKPPEENLYKSVAKSFKNPISPSS 1057
Db 1021 ECLKSGMDGYVSKPPEENLYKSVAKSFKNPISPSS 1057

RESULT 7
ABB91688
ID ABB91688 standard; Protein; 600 AA.
XX

AC ABB91688;
XX 31-MAY-2002 (first entry)
XX
DE Herbicidally active polypeptide SEQ ID NO 899.
XX
KW Herbicidal; plant; agriculture; herbicide.
XX
OS Arabidopsis thaliana.
XX
PN WO200210210-A2.
XX
PD 07-FEB-2002.
XX
PF 28-AUG-2001; 2001WO-EP09892.
XX
PR 28-AUG-2001; 2001WO-EP09892.
XX
PA (FARB) BAYER AG.
XX
PI Tietjen K, Weidler M;
XX
DR WPI; 2002-269010/31.
XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant
PT organisms -
XX
PS Claim 5; SEQ ID NO 899; 261pp + Sequence Listing; English.
XX
CC The invention relates to identifying target proteins
CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC aligning and comparing nucleic acid or amino acid sequences from plant
CC with nucleic acid or amino acid sequences from non-plant organisms using
CC suitable search parameters, where plant sequences having an E-value
CC greater by a factor of 3 than the E-value of most similar non-plant
CC sequences are selected. The polypeptides or nucleic acids encoding them
CC are useful for identifying modulators. The identified modulators are
CC useful as herbicides.
XX
SQ Sequence 600 AA;
Query Match 53.1%; Score 2865; DB 23; Length 600;
Best local Similarity 90.8%; Pred.No.1e-242;
Matches 575; Conservative 0; Mismatches 2; Indels 56; Gaps 2;
QY 424 MHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTELSSST 483
Db 1 MHIVKVEDDFHEMQELKVRAEAAADVAKSQFLATVSHEIRTPMNGILGMLAMLLDTELSSST 60
QY 484 QRDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSSESRNK 543
Db 61 QRDYAQTAQVCGKALIALINEVLDRAKIEAGKLELESVPFDIRSILDDVLSLFSSESRNK 120
QY 544 GIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDESEPK 603
Db 121 SIELAVFVSDKVPEIVKGDGRFRQIIINLVGNSVKFTEKGHIFVKVHLAEQSKDESEPK 180
QY 604 NALNGGVSEEMIVVSKQSSYNTLSGYEAAADGRNSWDSFKHLVSEEQSLSEFDISSNVRLM 663
Db 181 NALNGGV-----NVRLM 192
QY 664 VSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI SRP 723
Db 193 VSIEDTGIGIPLVAQGRVFMFPMQADSSTSRNYGGTGIGLSISKCLVELMRGQINFI SRP 252
QY 724 HIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAIVVDKPVRAAVTRYHMKR 783
Db 253 HIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTFKGMKAIVVDKPVRAAVTRYHMKR 312
QY 784 LGINVDVVTSLKTAVVAAAAAFERNGPSPLTPKPQLDMILVEKDSWISTEDNDSEIRLLNSR 843

Db	313	LGINVDVVTSLKTAVVAAAFERNGSPLPTKQOLDMILVEKDSWISTEDNDSEIRLLNSR	372	PR	25-MAY-1999;	99US-0136021.
				PR	27-MAY-1999;	99US-0136392.
QY	844	TNGNVHKKSPKIALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELRKTR	903	PR	28-MAY-1999;	99US-0136782.
				PR	01-JUN-1999;	99US-0137222.
Db	373	TNGNVHKKSPKIALFATNITNSEFDRAKSAGFADTVIMKPLRASMIGACLQQVLELRKTR	432	PR	03-JUN-1999;	99US-0137528.
				PR	04-JUN-1999;	99US-0137502.
QY	904	QOHPEGSSPATLKSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCABSGQVALGLLQI	963	PR	07-JUN-1999;	99US-0137724.
				PR	08-JUN-1999;	99US-0138094.
Db	433	QOHPEGSSPATLKSLLTGKKILVDDNIVNRRVAAGALKKFGAEVVCABSGQVALGLLQI	492	PR	10-JUN-1999;	99US-0138540.
				PR	10-JUN-1999;	99US-0138847.
QY	964	PHTFDACFMDIQMPQMDGFEATRQIRMEKEAKEKTNLEWHLPLILAMTADVIHATYEECL	1023	PR	14-JUN-1999;	99US-0139119.
				PR	16-JUN-1999;	99US-0139452.
Db	493	PHTFDACFMDIQMPQMDG-----MMEKETKEKTNLEWHLPLILAMTADVIHATYEECL	544	PR	16-JUN-1999;	99US-0139453.
				PR	17-JUN-1999;	99US-0139492.
QY	1024	KSGMDGYVSKPFEENLYKSVAKSFKNPISPS	1056	PR	18-JUN-1999;	99US-0139454.
				PR	18-JUN-1999;	99US-0139455.
Db	545	KSGMDGYVSKPFEENLYKSVAKSFKNPISPS	577	PR	18-JUN-1999;	99US-0139456.
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				PR	18-JUN-1999;	99US-0139458.
				PR	18-JUN-1999;	99US-0139459.
				PR	18-JUN-1999;	99US-0139460.
				PR	18-JUN-1999;	99US-0139461.
				PR	18-JUN-1999;	99US-0139462.
				PR	18-JUN-1999;	99US-0139463.
				PR	18-JUN-1999;	99US-0139750.
				PR	18-JUN-1999;	99US-0139763.
				PR	21-JUN-1999;	99US-0139817.
DE		Arabidopsis thaliana protein fragment SEQ ID NO: 59314.		PR	22-JUN-1999;	99US-0139899.
XX				PR	23-JUN-1999;	99US-0140353.
KW		Protein identification; signal transduction pathway; metabolic pathway;		PR	23-JUN-1999;	99US-0140354.
KW		hybridisation assay; genetic mapping; gene expression control; promoter;		PR	24-JUN-1999;	99US-0140695.
KW		termination sequence.		PR	28-JUN-1999;	99US-0140823.
XX				PR	29-JUN-1999;	99US-0140991.
OS		Arabidopsis thaliana.		PR	30-JUN-1999;	99US-0141287.
XX				PR	01-JUL-1999;	99US-0141842.
PN		EP10333405-A2.		PR	01-JUL-1999;	99US-0142154.
XX				PR	02-JUL-1999;	99US-0142055.
PD		06-SEP-2000.		PR	06-JUL-1999;	99US-0142390.
XX				PR	08-JUL-1999;	99US-0142803.
PF		25-FEB-2000; 2000EP-0301439.		PR	09-JUL-1999;	99US-0142920.
XX				PR	12-JUL-1999;	99US-0142977.
PR		25-FEB-1999;	99US-0121825.	PR	13-JUL-1999;	99US-0143542.
PR		05-MAR-1999;	99US-0123180.	PR	14-JUL-1999;	99US-0143624.
PR		09-MAR-1999;	99US-0123548.	PR	15-JUL-1999;	99US-0144005.
PR		23-MAR-1999;	99US-0125788.	PR	16-JUL-1999;	99US-0144085.
PR		25-MAR-1999;	99US-0126264.	PR	16-JUL-1999;	99US-0144086.
PR		29-MAR-1999;	99US-0126785.	PR	19-JUL-1999;	99US-0144325.
PR		01-APR-1999;	99US-0127462.	PR	19-JUL-1999;	99US-0144331.
PR		06-APR-1999;	99US-0128234.	PR	19-JUL-1999;	99US-0144332.
PR		08-APR-1999;	99US-0128714.	PR	19-JUL-1999;	99US-0144333.
PR		16-APR-1999;	99US-0129845.	PR	19-JUL-1999;	99US-0144334.
PR		19-APR-1999;	99US-0130077.	PR	19-JUL-1999;	99US-0144335.
PR		21-APR-1999;	99US-0130449.	PR	20-JUL-1999;	99US-0144352.
PR		23-APR-1999;	99US-0130510.	PR	20-JUL-1999;	99US-0144632.
PR		28-APR-1999;	99US-0130891.	PR	20-JUL-1999;	99US-0144884.
PR		30-APR-1999;	99US-0131449.	PR	21-JUL-1999;	99US-0144814.
PR		30-APR-1999;	99US-0132048.	PR	21-JUL-1999;	99US-0145086.
PR		30-APR-1999;	99US-0132407.	PR	21-JUL-1999;	99US-0145088.
PR		04-MAY-1999;	99US-0132484.	PR	22-JUL-1999;	99US-0145085.
PR		05-MAY-1999;	99US-0132485.	PR	22-JUL-1999;	99US-0145087.
PR		06-MAY-1999;	99US-0132486.	PR	22-JUL-1999;	99US-0145089.
PR		06-MAY-1999;	99US-0132487.	PR	22-JUL-1999;	99US-0145192.
PR		07-MAY-1999;	99US-0132863.	PR	23-JUL-1999;	99US-0145145.
PR		11-MAY-1999;	99US-0134256.	PR	23-JUL-1999;	99US-0145218.
PR		14-MAY-1999;	99US-0134218.	PR	23-JUL-1999;	99US-0145224.
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PR		18-MAY-1999;	99US-0134768.	PR	27-JUL-1999;	99US-0145918.
PR		19-MAY-1999;	99US-0134941.	PR	27-JUL-1999;	99US-0145919.
PR		20-MAY-1999;	99US-0135124.	PR	28-JUL-1999;	99US-0145951.
PR		21-MAY-1999;	99US-0135353.	PR	02-AUG-1999;	99US-0146386.
PR		24-MAY-1999;	99US-0135629.	PR	02-AUG-1999;	99US-0146388.
				PR	02-AUG-1999;	99US-0146389.

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QY 1045 AKSPKP 1050
|:|:|

Db 1126 ARFFEP 1131

RESULT 9

AAG47089

ID AAG47089 standard; Protein; 1176 AA.

XX

AC AAG47089;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 59313.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0130891.

PR 30-APR-1999; 99US-0131449.

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PR 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

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PR 14-MAY-1999; 99US-0134370.

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PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

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PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

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PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

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PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

PR 23-JUN-1999; 99US-0140353.

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PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

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PR 01-JUL-1999; 99US-0141842.

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PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

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PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

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PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

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PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.

PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147493.

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PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
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PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
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PR	21-OCT-1999;	99US-0160741.
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PR	22-OCT-1999;	99US-0160989.
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PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match 47.2%; Score 2546; DB 21; Length 1176;
Best Local Similarity 52.6%; Pred. No. 4.1e-214;
Matches 540; Conservative 156; Mismatches 244; Indels 86; Gaps 18;

QY	73	HSVAVKNNNNNDLMGNKKGSTFIOEHRALLPKAL-----ILWIIIV	115
Db	188	HKIYV-----SHSKARGERKEKVHLQE--ALAPKKQQQRAQTSSRGAGRWRKNILLGIL	240
QY	116	GFISSGIYQWDDANK---IRREEVLVSMCDQARMQLDQFVSVNHVHALAILVSTFHY	172

Db	241	GGVSFSVW-WFWDTNEEIIMKRRETLANCMDERARVLQDQFNVSNLHVHALSILVSTFHH	299
QY	173	HKNPSAIDQETFAEYTARTAFERPLLSGVAYAEKVYNFEREMFERQHWNVIKT-----	226
Db	300	GKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKKMETEDQT	359
QY	227	-----DRGEPSVRDEYAPVIFSQDSVSYLESDMMSGEEDRENILRARETGKAVLTS	279
Db	360	VVQDCVPENFDPAIQDEYAPVIFAQETVSHIVSDMMSGEEDRENILRARASGKVLTS	419
QY	280	PFRLLETHHLGVLTTFPVYKSSLPENPTVEERIAATAGYLGAFDVSLENLLQLAGN	339
Db	420	PFKLLKSNHLGVLTFAVYDTSLPPDATEEQRVEATIGYLGASYDMPSLVEKLLHLQASK	479
QY	340	QAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDGDPFRKHKMICRYHOKAPIPL	399
Db	480	QTIADVYDTTNTSGLIKMYGS--EIGDISEQHISSLDGDPSPRNHEMHCRCFKHKLPIPW	537
QY	400	NVLTTVPLFFAIGFLVGILYGAAMHIVKVEDDFHEMQELKVRAEAADVAKSOFLATVSH	459
Db	538	TAITPSILVLVITFLVGILYEAIRNIATVEEDCQKRELKARAEAAIAKSQFLATVSH	597
QY	460	EIRTPMNGILMLMLDTELSTORDYAQTAQVCGKALIALINEVLDRAKIHAQKLELE	519
Db	598	EIRTPMNGVLMLMLMDTDLDAKQMDYAQTAHSGKDLTSLINEVLDAQIESGRLELE	657
QY	520	SVPFDIRSILDDVLSLFSEESRNKGIELAVFVSDKVPEIVKGDGSRFRQIILNLVGSVK	579
Db	658	NVPFDMRFILDNVSSLLSGKANKEGIELAVYSSQVDPDVVGDPSPRFRQIITNLVGSIK	717
QY	580	FT-EKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQSSYNTLSGYEAADGRNSW	638
Db	718	FTQERGHIFISVHLADEVK---EPL-TIEDAVLKQRLALGCSEGETVSGFPVNAWGSW	773
QY	639	DSFKHLVSEEQSLSEFDISSNVRLMVSIEDTGIGIPLVAQGRVFMPEMQADSTSRNYGG	698
Db	774	KNFKTCYSTESQNSD-----QIKLLVTVEDTGVGIPVDAQGRIFTPEMQADSTSRTYGG	828
QY	699	TGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPST	758
Db	829	TGIGLSISKRLVELMQGEMGFVSEPGIGSTFSGTGVFGKAETNTSITKLER--FDLAIQE	886
QY	759	FKGMKAIIVVDKPVRAAVTRYHMKRLGINVDVVTSLKTAVVAAAAAFERNGSPLPTKPQLD	818
Db	887	FTGLRALVIDNENIRAEVTRYELRRLGISADIVSSLRMACTCCISKLEN-----LA	937
QY	819	MILVEKDSWISTEDNDSEIRLLNSR-TNGNV-HHKSPKLALFATNITNSEFDRAKSAGFA	876
Db	938	MILIDKDAW-----NKEEFSVLDELFTRSKVTFTRVPKIFLLATSATLTERSEMKTGLI	992
QY	877	DTVIMKPLRASMIGACLOQVLELRKTRQOHPEGSSPATLKSLLTGKKILVVDDNIVNRRV	936
Db	993	DEVVIKPLRMSVLICCLQETLVNGKKRQPNRQRN---LGHLREKQILVVDDNVLNRRV	1049
QY	937	AAGALKKFGAEVVCESGQVALGLLIQIPHTFDACFMDIOMPQMDGFEATRQIRMMEKEAK	996
Db	1050	AEGALKKYGAIVTCVESGKAALAMLPKPHNFDACFMDLQMPEMDGFETRVRRELEREIN	1109
QY	997	EKTN-----LEWHLPILAMTADVIHATYEECLKSGMDGYVSKPFEENLYKSV	1044
Db	1110	KKIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEEEVLYTAV	1169
QY	1045	AKSFKP	1050
Db	1170	ARFFEP	1175
RESULT 10			
ABG70781			
ID	ABG70781	standard; Protein; 1176 AA.	
XX			
AC	ABG70781;		

DT	16-APR-2003	(first entry)
XX	Arabidopsis thaliana histidine kinase 2 (AHK2) protein.	
DE	Shoot formation; senescence; transgenic; transgenic plant; agriculture;	
XX	cell proliferation; shoot meristem formation; leaf development; AHK;	
KW	photosynthesis; histidine kinase; enzyme.	
KW	Arabidopsis thaliana.	
XX	WO200299079-A2.	
XX	12-DEC-2002.	
XX	06-JUN-2002; 2002WO-US18066.	
PF	06-JUN-2001; 2001US-296554P.	
XX	(GEO) GEN HOSPITAL CORP.	
PA	Sheen J, Hwang I;	
XX	WPI; 2003-140613/13.	
DR	N-PSDB; AAD51604.	
XX	Increasing yield in plant, increasing shoot formation in a plant, or	
PT	delaying senescence in a plant such as wheat, rice, maize, barley,	
PT	potato, by using transgenes that regulate cytokinin response	
XX	Disclosure; Page 75-78; 87pp; English.	
PS	The present invention relates to a novel method of increasing yield in a	
XX	plant, increasing shoot formation or delaying senescence in a plant. The	
CC	method involves introducing into plant cells, a transgene having a B-type	
CC	response regulator operably linked to a promoter functional in plant	
CC	cells to yield transformed plant cells or whose expression reduces the	
CC	expression of A-type response regulator in the cells of the plant and	
CC	regenerating a plant from the transformed cells. The method is useful	
CC	for increasing the yield in a plant, increasing the shoot formation or	
CC	delaying senescence in a plant such as wheat, rice, maize, barley,	
CC	potato, tomato, soybean, oat, cotton and sunflower. The method	
CC	is useful for variety of agricultural and commercial purposes including	
CC	improving and enhancing photosynthesis, promoting cell proliferation,	
CC	shoot meristem formation, promoting leaf development, increasing crop	
CC	yields, improving crop and ornamental quality and reducing agricultural	
CC	production costs. The present sequence is Arabidopsis thaliana histidine	
CC	kinase 2 (AHK2) protein. This sequence is used to illustrate the method	
CC	of the invention.	
XX	Sequence 1176 AA;	
SQ	Query Match 47.2%; Score 2546; DB 24; Length 1176;	
	Best Local Similarity 52.6%; Pred. No. 4.1e-214;	
	Matches 540; Conservative 156; Mismatches 244; Indels 86; Gaps 18;	
QY	73 HSAVAKNNNNNDLGNKKGSTFIOEHRALLPKAL-----ILWIIIV 115	
DB	188 HKIYV-----SHSKARGERKEKVLQE--ALAPKQQQRAQTSSRGARWRKNILLGIL 240	
QY	116 GFISGGIYQWDDANK---IRREEVLVSMCDQARMLQDQFSVNVHVALAILVSTFHY 172	
DB	241 GGVSFVW-WFWDNTEIIMKRRETLANMCDERARVLQDQFNVLNHHVALSILVSTFHH 299	
QY	173 HKNPSAIDQETFAEYARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKT----- 226	
DB	300 GKIPSAIDQRTFEEYTERINFERPLTSGVAYALKVPHSEREKEFEHGWAKKMETEDQT 359	
QY	227 -----DRGEPSVRDEYAPVIPSQDSVSYLESIDMSGEEDRENILRARETGKAVLTS 279	
DB	360 VVQDCVPENFDPAIQDEYAPVIFAQETVSHIVSDMSGEEDRENILRARASGKGLTS 419	
QY	280 PRLLETHLGLVLTFFPVYKSSSLPENPTVEERIAATAGYLGAFDVSLENLLGQLAGN 339	

PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
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PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.

PR	23-SEP-1999;	99US-0155486.	
PR	24-SEP-1999;	99US-0155659.	
PR	28-SEP-1999;	99US-0156458.	
PR	29-SEP-1999;	99US-0156596.	
PR	04-OCT-1999;	99US-0157117.	
PR	05-OCT-1999;	99US-0157753.	
PR	06-OCT-1999;	99US-0157865.	
PR	07-OCT-1999;	99US-0158029.	
PR	08-OCT-1999;	99US-0158232.	
PR	12-OCT-1999;	99US-0158369.	
PR	13-OCT-1999;	99US-0159293.	
PR	13-OCT-1999;	99US-0159294.	
PR	13-OCT-1999;	99US-0159295.	
PR	14-OCT-1999;	99US-0159329.	
PR	14-OCT-1999;	99US-0159330.	
PR	14-OCT-1999;	99US-0159331.	
PR	14-OCT-1999;	99US-0159637.	
PR	14-OCT-1999;	99US-0159638.	
PR	18-OCT-1999;	99US-0159584.	
PR	21-OCT-1999;	99US-0160741.	
PR	21-OCT-1999;	99US-0160767.	
PR	21-OCT-1999;	99US-0160768.	
PR	21-OCT-1999;	99US-0160770.	
PR	21-OCT-1999;	99US-0160814.	
PR	21-OCT-1999;	99US-0160815.	
PR	22-OCT-1999;	99US-0160980.	
PR	22-OCT-1999;	99US-0160981.	
PR	22-OCT-1999;	99US-0160989.	
PR	25-OCT-1999;	99US-0161404.	
PR	25-OCT-1999;	99US-0161405.	
PR	25-OCT-1999;	99US-0161406.	
PR	26-OCT-1999;	99US-0161359.	
PR	26-OCT-1999;	99US-0161360.	
PR	26-OCT-1999;	99US-0161361.	
PR	28-OCT-1999;	99US-0161920.	
PR	28-OCT-1999;	99US-0161992.	
PR	28-OCT-1999;	99US-0161993.	
PR	29-OCT-1999;	99US-0162142.	
Query Match 47.2%; Score 2546; DB 21; Length 1238;			
Best Local Similarity 52.6%; Pred. No. 4.5e-214;			
Matches 540; Conservative 156; Mismatches 244; Indels 86; Gaps 18;			
QY	73	HSVAVKMNNNNDLMGNKKGSTFIOEHRALLPKAL-----ILWIIIV	115
Db	250	HKIYV-----SHSKARGEKKEKVHLQE--ALAPKKQOQRAQTSSRGAGRWRKNILLGIL	302
QY	116	GFISSGIYQWDDANK---IRREEVLVSMCDQARMQLQDQFSVSNHVHALAILVSTFHY	172
Db	303	CGVSFSVW-WFWDTNEEIIMKRRETLANMCDERARVLQDQFNVSLNHVHALSILVSTFHH	361
QY	173	HKNPSAIDQETFAEYFARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTM-----	226
Db	362	GKIPSAIDQRTFEEYTERTNFERPLTSGVAYALKVPHSEREKFEKEHGWAIKQMETEDQT	421
QY	227	-----DRGEPSPVRDEYAPVIFSQDSVSYLESLDMSGEEDRENILRARETGKAVLTS	279
Db	422	VVQDCVPENFDPAPIQDEYAPVIFAQETVSHIVSDVMSGEEDRENILRARASGKGLTS	481
QY	280	PFRLLETHLGVLTFFPVYKSSLPENPTVEERIAATAGYLGAFDVESLVENLLGQLAGN	339
Db	482	PFKLLKSNHLGVLTFAVYDTSLLPDATEEQRVEATIGYLGASYDMPSLVEKLLHLQASK	541
QY	340	QAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPL	399
Db	542	QTIADVYDITNTSGLIKMYGS--EIGDISEQHISSLDFGDPDSRNHEMCHRFKHLPIPW	599
QY	400	NVLTTPVLPFFAIGFLVGILYGAAMHIVKVEDDFHEMQELKVRAEAADVAKSQFLATVSH	459
Db	600	TAITPSILVLVITFLVGILYEAINRIATVEEDCQKMKELKARAEAAADIAKSQFLATVSH	659
QY	460	EIRTPMNGILGMLAMLLDTELSSTQRDYAOQAQVCGKALIALINEVLDRAKIEAGKLELE	519

Db	660	EIRTPMNGVLGMLMDTDLDAKQMDYAQTAHGGSKDLTSLINEVLDQAKIESGRILELE	719
QY	520	SVPFDIRSILDVLSFSEESRNKGIELAVFVSKVPEIVKGDGSRFRQIIINLVGNSVK	579
Db	720	NVPFDMRFILDNVSSLLSGKANEGIELAVYVSSQVPDVVVGDPSPRFRQIITNLVNSIK	779
QY	580	FT-EKGHIFVKVHLAEQSKDESEPKNALNGGVSEEMIVVSKQSSYNTLSGYEAADGRNSW	638
Db	780	FTQERGHIFISVHLADEVK--EPL-TIEDAVLKQRLALGCSEGETVSGFFPAVNAWSW	835
QY	639	DSFKHLVSEEQSLSEFDISSNVRLMVSIEDTGIGIPLVAOGRVFMFPMQADSSTSRNYGG	698
Db	836	KNFKTCYSTESQNSD-----QIKLLVTVEDTGVGIPVDAQGRIFTFFMQADSSTRTYGG	890
QY	699	TGIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPST	758
Db	891	TGIGLSISKRLVELMQEMGFVSEPGIGSTFSFTGVFGKAETNTSITKLER--FDLAIQE	948
QY	759	FKGMKAIVVDKPVRAAVTRYHMKRLGINVDVVTSLKTAVVAAAAFERNGSPLPKQLD	818
Db	949	FTGLRALVIDNRNIRAETRYELRRLGISADIVSSLRMACTCCISKLEN-----LA	999
QY	819	MILVEKDSWISTEDNDSEIRLLNSR-TNGNV-HHKSPKLALFATNITNSEFDRAKSAGFA	876
Db	1000	MILIDKDAW-----NKEEFSVLDELFTRSKVTFTTRVPKIFLLATSATLTERSEMKSTGLI	1054
QY	877	DTVIMKPLRASMIGACLQOVLELRKTRQOHPGESSPATLKSLLTGKKILVDDNIVNRRV	936
Db	1055	DEVVIKPLRMSVLICLQETLVNGKKRQPNQRN---LGHLLREKQILVDDNIVNRRV	1111
QY	937	AAGALKKFGAEVVCESGQVALGLLQIPHITDACPMDIQMPQMDGFEATQIRMMKEAK	996
Db	1112	AEGALKKYGAIVTCVESGKAALAMLKPPHNFDAFCFMDLQMPENDGFEATRVRELEREIN	1171
QY	997	EKTN-----LEWHLPILAMTADVTHATYEECLKSGMDGYVSKPPEENLYKSV	1044
Db	1172	KKIASGEVSAEMFCFSSWHVPILAMTADVIQATHEECMCGMDGYVSKPPEEVLYTAV	1231
QY	1045	AKSFKP	1050
Db	1232	ARFFEP	1237
RESULT 13			
AAO22568	ID	AAO22568	standard; Protein; 1173 AA.
XX	AC	AAO22568;	
XX	DT	28-OCT-2002	(first entry)
XX	DE	Wooden leg (WOL)	gene related protein SEQ ID No 19.
XX	KW	Wooden leg; WOL;	vasculature; transgenic plant; agronomic; longer root;
XX	KW	wood production; plant;	promoter; tree; crop plant.
XX	OS	Arabidopsis	thaliana.
XX	PN	WO200244337-A2.	
XX	PD	06-JUN-2002.	
XX	PF	29-NOV-2001;	2001WO-US45053.
XX	PR	29-NOV-2000;	2000US-253739P.
PA		(UJNY)	UNIV NEW YORK STATE.
PA		(HELA/)	HELARIUTTA Y.
PA		(MAHO/)	MAHONEN A P.
PA		(BONK/)	BONKE A W M.
PA		(KAUP/)	KAUPPINEN L.
XX		(RIIK/)	RIIKONEN M.

PI Helariutta Y, Mahonen AP, Bonke AWM, Kauppinen L, Riikonen M;
PI Benfey PN;
XX
DR WPI; 2002-599423/64.
XX
PT Novel isolated polypeptide (WOODEN LEG) with ability to regulate a set
PT of asymmetric cell divisions that establish vascular tissue in root and
PT hypocotyl development, useful for improving agronomically valuable
PT plants -
XX
XX Example 1; Page 161-164; 187pp; English.
PS
XX The invention relates to an isolated WOODEN LEG (WOL) polypeptide,
CC comprising 15 contiguous amino acids of a fully defined Arabidopsis
CC WOODEN LEG protein sequence of 1057 amino acids as given in the
CC specification, and to its encoding nucleic acid. The invention also
CC relates to an amino acid sequence of domains of protein, e.g., N-terminal
CC region, C-terminal domain, etc; or is a naturally occurring allelic
CC variant of the above mentioned polypeptide sequence. Expression levels of
CC the nucleic acid can be modified to improve the vasculature in transgenic
CC plants and enhance the agronomic properties of such plants. Also the WOL
CC promoter is used to drive expression of a heterologous coding sequence of
CC trees to improve wood production. The WOL nucleic acid may be used as a
CC molecular marker for a qualitative trait loci, e.g., longer roots or
CC enhanced wood production, in molecular breeding of crop plants. The
CC nucleic acid is also useful in DNA amplification assays to identify the
CC endogenous WOL genes, WOL mutant alleles and/or WOL expression products
CC in cultivars as compared to wild-type plants. They can also be used as
CC markers for linkage analysis of qualitative trait loci. The WOL protein
CC and/or antibodies can be used as diagnostic reagents in immunoassays to
CC detect expression of the WOL gene in cultivars and wild-type plants. The
CC WOL protein, its encoding nucleic acid, and its corresponding antibody
CC are useful for improving agronomically valuable plants e.g., trees. This
CC sequence represents a protein relating to the wooden leg (WOL) protein of
CC the invention.
XX
SQ Sequence 1173 AA;

Query Match 47.0%; Score 2534.5; DB 23; Length 1173;
Best Local Similarity 52.5%; Pred. No. 4.2e-213;
Matches 538; Conservative 156; Mismatches 244; Indels 87; Gaps 18;

QY 73 HSAVAVKMNNDLMGNKKGSTFQIEHRALLPKAL-----ILWIIIV 115
Db 188 HKIYV-----SHSKARGERKEKVLQE--ALAPKKQQQAQTSRGAGRWKNNILLGIL 240
QY 116 GFISGIYQWDDANK--IRREEVLVSMCDQARMQLQDFSVSNVHVALAILVSTFHY 172
Db 241 GGVSFSVW-WFWDTNEEIIIMKRRETLANMCDERARVLQDFNVSLNHVHALSILVSTFHH 299
QY 173 HKNPSAIDQETFAEYTAARTAFERPLLSGVAYAEKVNVFEREMFERQHNWVIKTM----- 226
Db 300 GKIPSAIDQRTFEYTERTNFRPLTSGVAYALKVPHSEREKFEKEHGWAIKGMETEDQT 359
QY 227 -----DRGEPSPVRDEYAPVIFSQDSVSYLESLDMMSGEEDRENILRARETGKAVLTS 279
Db 360 VVQDCVPENFDPAIQDEYAPVIFAQETVSHIVSVDMMSGEEDRENILRARASGKGLTS 419
QY 280 PFRLLETHHLGVVLTFFPVYKSSLPENPTVEERIAATAGYLGGAFDVESLVENLLGQLAGN 339
Db 420 PFKLLKSNHLGVVLTFAVYDTSLPDPATEEQRVEATIGYLGASYDMPSLVEKLLHLQASK 479
QY 340 QAIVVHVVDITNASDPLVMYGNQDEEADRSLSHESKLDGDFGDFPKHKMKICRYHQKAPIPL 399
Db 480 QTIADVVDTTNTSGLIKMYGS--EIGDISEQHISSLDGDFGDFSRNHMHCRFKHKLPIPW 537
QY 400 NVLTTVPLFFAIGFLVGYILYGAAMHIVKVVEDDFHEMQELKVRAEAAADVAKSQFLATVSH 459
Db 538 TAITPSILVIVITFLVGYILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSH 597
QY 460 EIRTPMNGILGMLAMDLDTELSSTQDYAQTAQVCGKALIALINEVLDRAKIEAGKLELE 519
Db 598 EIRTPMNGVLGMLKMLMDTDLDAKQMDYATAGSGKDLTSLINEVLDQAKIESGRLELE 657

QY 520 SVPFDIRSILDDVLSLFSSESRNKGIELAVFVSDKVPEIVKGDGSRFRQIILNVGNSVK 579
Db 658 NVPFDMRFILDNVSSLLSGKANEGIELAVVYSSQVDPVVVGDPSRFRQIITNLVGNISIK 717
QY 580 FTEKGHIFVKVHLAEQSKDESEPKNALNGVSEEMIVVSKQSSYNTLSGYEADGRNSWD 639
Db 718 --ERGHIFISVHLADEVK--EPL-TIEDAVLKQRLALGCSEGETVSGFPAVNAWGSWK 771
QY 640 SFXHLVSEEQSLSEFDISSNVRLMVSIEDTGIGIPLVAQGRVPMFQMADSSSTRNYGGT 699
Db 772 NEKTCYSTESQNSD-----QIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSSSTRTYGGT 826
QY 700 GIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKKPNVEHLPSTF 759
Db 827 GIGLSISKRLVELMQGEMGFVSEPGIGSTFSFTGTGFGKAEINTSITKLER--FDLAIQEF 884
QY 760 KGMKAIVVDAKPVRAAVTRYHMKRLGINVDVVTSLKTAVVAAAAAFERNGSPLPTKPQLDM 819
Db 885 TGLRALVIDNRNIRAEVTRYELRRLGISADIVSSLRMACTCCTCKLEN-----LAM 935
QY 820 ILVEKDSWISTEDNDSEIRLLNSR-TNGNV-HHKSPKLALPATNITNSEFDRAKSAGFAD 877
Db 936 ILIDKDAW-----NKEEFSVLDELFTRSKVTFTTRVPKIFLLATSATLTERSEMKTGLID 990
QY 878 TVIMKPLRASMIGACLOQVLELRKTRQOHPEGSSPATLKSLLTGKKILVDDNIVNRRVA 937
Db 991 EVVIKPLRMSVLICCLQETLVNCKKQPNRQRN---LGHLLREKQILVDDNLVNRVA 1047
QY 938 AGALKKFGAEVCAESGGQVALGLLQIPHFTFDACFMDIQMPQMDGFEATRQIRMMEKEAKE 997
Db 1048 EGALKKYGAIVTCVESGKAALAMLKPPHNFDA CFMDLQMBMDGFEATRRVRELEREINK 1107
QY 998 KTN-----LEWHLPLAMTADVIHATYEECLSGMDGYVSKPFEEENLYKSA 1045
Db 1108 KIASGEVSAEMFCKFSSWHVPILAMTADVIQATHEECMKCGMDGYVSKPFEEVLYTAVA 1167
QY 1046 KSFKP 1050
Db 1168 RFPEP 1172

RESULT 14

ABB93625
ID ABB93625 standard; Protein; 1173 AA.

XX
AC ABB93625;

XX
DT 31-MAY-2002 (first entry)

XX
DE Herbicidally active polypeptide SEQ ID NO 2836.

XX
KW Herbicidal; plant; agriculture; herbicide.

XX
OS Arabidopsis thaliana.

XX
PN WO200210210-A2.

XX
PD 07-FEB-2002.

XX
PF 28-AUG-2001; 2001WO-EP09892.

XX
PR 28-AUG-2001; 2001WO-EP09892.

XX
PA (FARB) BAYER AG.

XX
PI Tietjen K, Weidler M;

XX
DR WPI; 2002-269010/31.

XX
PT Identifying plant target proteins for herbicidally active compounds,
PT comprising aligning and comparing nucleic acid or amino acid sequences
PT from plant with nucleic acid or amino acid sequences from non-plant

organisms -
Claim 5; SEQ ID NO 2836; 261pp + Sequence Listing; English.
The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
Sequence 1173 AA;
Query Match 47.0%; Score 2534.5; DB 23; Length 1173;
Best Local Similarity 52.5%; Pred. No. 4.2e-213;
Matches 538; Conservative 156; Mismatches 244; Indels 87; Gaps 18;
QY 73 HSAVKMNNNNNDLMGNKKGSTFIQEHRAALLPKAL-----ILWIIIV 115
Db 188 HKIIV-----SHSKARGERKEKVKHLQE--ALAPKKQQQRAQTSSRGAGRWRKNILLGIL 240
QY 116 GFISGGIYQWDDANK---IRREVLVSMCDQARMLOQFSVSNVHVHALAILVSTFHY 172
Db 241 GGVSFVW-WFWDTNEEIIIMKRRETLANMCDERARVLQQFNVSILNVHVALSILVSTFFH 299
QY 173 HKNPSAIDQETPAEYRTARTAFERPLLGGVAYAEKVNVFEREMFERQHNWVIKTM----- 226
Db 300 GKIPSAIDQRTFEYTERTFNFRPLTSGVAYALKVPHSREKFEKEHGWAIKKMETEDQT 359
QY 227 -----DRGEPSPVRDEYAPVIFSQDSVSYLESIDMMSGEEDRENILRARETGKAVLTS 279
Db 360 VVQDCVPENFDPAPIQDEYAPVIFAQETVSHIVSVDMMSGEEDRENILRARASGKVLTS 419
QY 280 PFRLLETHLGVLTFFPVYKSSLPENPTVEERIAATAGVLGAFDVESLVENLLGQLAGN 339
Db 420 PFKLLKSNHLGVLTFAVYDTSLPDPDATEEQRVEATIGLASYDMPSLVEKLLHLQASK 479
QY 340 QAIVVHVYDITNASDPLVMYGNQDEEADRSLSHESKLDGDPFRKHKMICRYHQKAPIPL 399
Db 480 QTIADVYDTTNTSGLIKMYS--EIGDISEQHIISSLDGDPSPRNHEMHCRFKHKLPIW 537
QY 400 NVLTTVPLFFAIGFLVGXILYGAAMHIVKVEDDFHENQELKVRAEAAADVAKSQFLATVSH 459
Db 538 TAITPSILVLVITFLVGXILYEAINRIATVEEDCQKRELKARAEAAADIAKSQFLATVSH 597
QY 460 EIRTPMNGILMLAMDTELSSTQDYAQTAVCGKALIALINEVLDRAKIRAGKLELE 519
Db 598 EIRTPMNGVLGMLKMLMDTDLDAKQMDYAQTAGSGKDLTSLINEVLDQAKIESGRLELE 657
QY 520 SVPFDIRSILDVLSFSEESRNKGIELAVFVSDKVPEIVKDGSRFRQIINLVGNSVK 579
Db 658 NVPFDMRFILDNVSSLLSGKANEGIELAVYVSSQVPDVVVGDPSPRFRQIITNLVNSIK 717
QY 580 FTEKGHIFVKVHLAEQSKDSEPKNALNGGVSEEMIVVSKQSSYNTLSGYEADGRNSWD 639
Db 718 --ERGHIFISVHLADEVK--EPL-TIEDAVLKQRLALGCSEGETVSGFFAVNAWSWK 771
QY 640 SPKHLVSEEQSLSEFDISSNVRLMVSIEDTGIGIPLVAQGRVFMFPMQADSTSRNYGGT 699
Db 772 NFKTCYSTESQNSD-----QIKLLVTVEDTGVGIPVDAQGRIFTFPMQADSTSRTYGGT 826
QY 700 GIGLSISKCLVELMRGQINFISRPHIGSTFWFTAVLEKCDKCSAINHMKPNVEHLPSTF 759
Db 827 GIGLSISKRLVELMQGMGFVSEPGIGSTFSTGTFPGKAETNTSITKLER--FDLAIQEF 884
QY 760 KGMKAIVVDKPVRAAVTRYHMKRLGINVDVVTSLKTAVVAAAFAERNGSLPTKPLQDM 819
Db 885 TGLRALVIDNRNIRAEVTRYELRRLGISADIVSLRMACTCCISKLEN-----LAM 935
QY 820 ILVEKDSWISTEDNDSEIRLLNSR-TNGNV-HKSPKALFATNITNSEFDRAKSAGFAD 877

Db 936 ILIDKDAW-----NKEEFSVLDELFTRSKVTFTTRVPKIFLLATSATLTERSEMKSTGLID 990
QY 878 TVIMKPLRASMIGACLOQVLELRKTRQOHPEGSSPATLKSLLTGKKILVVDDNIVNRRVA 937
Db 991 EVVIKPLRMSVLICCLQETLVNGKKRQPNRQRN---LGHLREKQILVVDDNLVNRVA 1047
QY 938 AGALKKFGAEVVCESGQVALGLLQIPHTFDACFMDIQMPQMDGFEATRQIRMEKEAKE 997
Db 1048 EGALKKYGAIVTCVESGKAALAMLKPPHNFACFMDLQMPMDGFEATRRVRELEIREINK 1107
QY 998 KTN-----LEWHLPILAMTADVIHATYEELKSGMDGYVSKPFEEENLYKSVA 1045
Db 1108 KIASGEVSAEMFCFSSWHVIPILAMTADVIQATHEECMCKGMDGYVSKPFEEVLYTAVA 1167
QY 1046 KSFKP 1050
Db 1168 RFFEP 1172
RESULT 15
ABG70782
ID ABG70782 standard; Protein; 1036 AA.
XX
AC ABG70782;
XX
DT 09-DEC-2002 (first entry)
XX
DE A. thaliana cytokinin receptor, AHK3, protein.
XX
KW AHK3; plant; antagonist; agonist; cytokinin receptor;
KW receptor; signal transduction; histidine kinase; hormone; cell division;
KW cell differentiation; agriculture; growth regulator; harvest.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT Region 32..1036
FT /note= "This region is specifically claimed in Claim 1"
XX
PN EP1241182-A2.
XX
PD 18-SEP-2002.
XX
PF 13-MAR-2002; 2002EP-0005749.
XX
PR 15-MAR-2001; 2001JP-0073812.
PR 29-JUN-2001; 2001JP-0198639.
PR 29-JUN-2001; 2001JP-0198640.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Kakimoto T, Higuchi M, Inoue T;
XX
DR WPI; 2002-693041/75.
DR N-PSDB; ABS54451.
XX
PT Analyzing agonist or antagonist activity of a substance for use as a
PT plant growth regulator, comprises measuring intracellular signal
PT transduction from a cytokinin receptor expressed in a cell contacted
PT with the test substance -
XX
PS Claim 1; Page 32-34; 47pp; English.
XX
CC The invention discloses a method for analysing antagonist or agonist
CC activity to a cytokinin receptor. The method comprises bringing a
CC candidate substance into contact with a transformed cell, in which a DNA
CC encoding the receptor has been introduced, and then measuring the
CC existence, or the quantity, of the intracellular signal transduction from
CC the receptor expressed in the cell. The cytokinin receptor comprises an
CC extracellular region of the receptor, transmembrane regions, a histidine
CC kinase region and a receiver region of the kinase. The transmembrane
CC regions and kinase region are homogeneous to each other and the receptor

